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Sequence 18, Appl
Sequence 1585, Ap
Sequence 299, App
Sequence 20447, A
Sequence 51438, A
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Sequence 46, Appli
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Sequence 321, App
Sequence 2119, Ap
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Sequence 92, Appl
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                                                                                                                                                       March 11, 2004, 03:37:21; Search time 353.257 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1438 Sequence 51. Sequence 241. 3898 Sequence 13. 3898 Sequence 13. 88352 Sequence 48.	## ###################################	463A1 1303785CB1 DB 9, Length 1516,	0; Indels AAACAGAAGGCAGCCA
S US-10-242-53 US-09-864-864 US-10-085-78 US-10-242-53 US-10-085-78	103-042-535A-103-045-701-564-134-134-134-134-134-134-134-134-134-13	Dher M. CANCER MARKERS US/09/919,172 77-30 7/222,469 28 ID No. US20020119 7 9, or other 7 Score 1515;	; Pred. No. 0; 0; Mismatches CTGAGCCATGTACTT
8.55 6 60 6 6 1 4 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 1 8 6 6 6 6	38.000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	nn US/ 1341 (contributed to the contributed to the	milarity 100. Conservative TTTGTTTTTGGACAT
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44440	n n	RESULT 1 SACTO 1 SACTO 1 APPR 1 TIT 1 T	Ma Ma

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1 CTTGTTTTTGGACATAGCTGAGCCATGTACTTCAAACAGAAGGCAGCCAATTACTAACT 60

OY 1201 TATGAGAAATCCTGGTGCTCTTTGTGAAGAACTTAAACATTCCCTTGATGGTCGAACTCCTTGATGGTCGTCTAA 126 Db 1201 TATGAGAAAATCCTGGTGGTCTTTTTTTTTTTTTTTTTT	RESULT 2 US-09-74-298-92 US-09-74-298-92 Sequence 92, Application US/09974298 Sequence 92, Application US/09974298 Sequence 92, Application US/09974298 Patent No. US20020156263A1 GENERAL INFORMATION TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER FILE REFERENCE: PA-0037 P CURRENT APPLICATION NUMBER: US/09/974,298 CURRENT FILING DATE: 2001-10-04 PRIOR PILING DATE: 2001-10-04 PRIOR PILING DATE: 2000-05-10 NUMBER OF SEQ ID NOS: 194 SOFTWARE: PREL PROGram SEQ ID NO 92 LENGTH: 1516 TYPE: DNA ORGANISM: Homo sapiens PEATURE:	NAME/KEY: MISCRETAINER NAME/KEY: MISCRETAINER NAME/KEY: MISCRETAINER NAME/KEY: UNSURE NAME/KEY: UNSURE NAME/KEY: UNSURE NAME/KEY: UNSURE NAME/KEY: UNSURE NAME/KEY: UNSURE OTHER INFORMATION: a, t, c, g, or other OTHER INFORMATION: a, c, c, g, or other OTHER I
121 TGCCAGGGGAAATCTTCAGAGAATTTCTCTTTAGTTCTTTGCAAGAGAGAG	481 ACACTGAAGAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTTAGCTCTGCTAAAACT 540 481 ACACTGAAGAAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTTAGCTCTGCTAAAACT 540 481 ACACTGAAGAAAAGCCCTTACAGGTCACCTTGAGGAGGTTGTTTTAGCTCTGCTAAAAACT 540 541 CCAGCGCAATTTGATGAAGTTGGTGCTGCCATGAAGGGCCTTGGAACTCATGAA 600 541 CCAGCGCAATTTGATGAAGTTGGTGCTGCCATGAAGGGCCTTGGAACTCATGAA 600 601 GATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAAATCAGAGAACTTAAACAG 660 601 GATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAAAATCAGAGAACATTAACAGG 660 661 GTCTACAGAAGGAACTGAAGAAACTAACAAAGAAAAAACTCAGACAATTAACAGG 660 661 GTCTACAGAAGGAACTGAAGAAACTGACCAAAGAAAAACTCAGACAATTGGGA 720 721 GATTTTCGAAGAGAACTTGCTTGCTAAGGGAGACATTTGGTGTG 780 721 GATTTTCGGAACGCTTTGCTTAGCTAAGGGTGACCGATCTGAGGACTTTTGGTGTG 780 721 GATTTTCGGAACGCTTTGCTTAGCTAAGGGTGACCGATCTGAGGACTTTTGGTGTG 780 721 GATTTTCGGAACGCTTTGCTTAGCTAAGGGTGACCGATCTGAGGACTTTTGGTGTG 780	781 781 841 901 901 961 1021 1021 1081 1081
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	GCTATGATCAGAAGACTTTAATTATATATTTCATCCTATAAGCTTAAALAGGAAAGTTT 	gaaaaatatagccttt 	TTTTTAAAAATGTTT TTTTTAAAATGTTT	CATGAGAAGATGTCT 		CANCER	63A1 1303785CB1	B 9; Length 1516 0; Indels	aacagaaggcagccab 	ataaaatcagaagccca 	ttagttctttgcaagaz 	aatteeteaageaggee 	AGTCATCCAAAGGTGGT
	AATTATATATTTTCAT 	TAGCTACCTACATGCT	aatagagataagtcca aatagagataagtcca	TGTTCTAGTAACAATA TGTTCTAGTAACAATA	16 16	974298 RESSED IN BREAST S/09/974,298 -04 238,331	No. US2002015626 g, or other	Score 1515; D Pred. No. 0; 0; Mismatches	CTGAGCCATGTACTTCA	CTTCCTTTAAATCCT/	agagaagaatticici agagaagaatticici	atggcaatggtatcag; atggcaatggtatcag;	PATGTTCAAACTGTGA
	TATGATCAGAAGACIII 	CITCAACAGGAITACAGTGTAGCTACCTACATGCTGAAAATATAGCCTTTAAATCATTT 	TTATATTATAACUCTGTATAATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAAC 	Cataaaaccctatacaagttgttctagtaacaatacatgagaagatgtctatgtgggtg 	AAAATAAAATGNCGTC 15 	us/09 11 11 12 13 13 14 10 10 10 10 10 10 10 10 10 10 10 10 10	TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID NAME/KEY: unsure IOCATION: 1512 OTHER INFORMATION: a, t, c, 6.09-974-298-92	y Match 99.9%; Local Similarity 100.0%; hes 1516; Conservative	CITIGITITIGGACAIAGCIGAGCCAIGTACTICAAACAGAAGGCAGCCAATTACTAACT 	tctggttgctaggtgtggcttcctttaaaatcctataaaatcagaagcccaagtctcac 	tgccagtgtgaaatcttcagagaagaatttctctttagttctttgcaagaaggtagat 	aargacactititicaaaatggcaatggtaatcagaattccccaagcaggcctggttatt 	GAAAATGAAGGGGGGAAATATGTTCAAACTGTGAAGGTCATCCAAAGGTGGTCCGGGATCA
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1201 TATGAGAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260 1261 GCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320 1321 CTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAAATATAGCCTTTAAATCATTT 1380 1380 1381 TTATATTATAACTCTGTATAATAGAGATAAGTCCATTTTTAAAAATGTTTTCCCCAAAC 1440 1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500 ö 1201 TATGAGAAATCCTGGTGGCTCTTTGTGGAGGAAACTAAACATTCCCTTGATGGTCTCAA 1260 1261 GCTATGATCAGAAGACTTTAATTATATTTTCATCCTATAAGCTTAAATAGGAAAGTTT 1320 121 reccaereraaarerreagagaagaarrrererragirerregaagaagaragaar 180 241 GAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCGGATCA 300 TGCCAGTGTGAAATCTTCAGAGAAGTTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGAT 180 181 AAAGACACTITITCAAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATT 240 181 AAAGACACTTTTTCAAAATGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATT 240 61 TCTGGTTGCTAGGTGTGGCTTCCTTTAAAATCCTATAAAATCAGAAGCCCAAGTCTCCAC 120 61 reregriserragererectirrahahrectarahahreagaheedeaheredeke 120 1 cringiriringaacanagcigagccangrachicaaacagaaggcagccaarnachaach 60 1 CITIGITITIGGACATAGCIGAGCCAIGIACTICAAACAGAAGGCAGCCAATTACTAACT 60 1321 CTTCAACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTT 0; Gaps Query Match

99.9%; Score 1515; DB 9; Length 1516;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1516; Conservative 0; Mismatches 0; Indels 0; NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20020156263A1 1303785CB1 Sequence 92, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INPORMATION
; APPLICANT: Chen, Huei-Mei
; ITLLE OF INVENTION: GENES EXPRESSED IN BEARST CANCER
; THERE REPERENCE: PA-0037
; CURRENT APPLICATION NUMBER: L9-097974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-04
; RIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194 OTHER INFORMATION: a, t, c, g, or other IS-09-974-298-92 1501 AAAATAAATGNCGTC 1516 SOFTWARE: PERL Program
SEQ ID NO 92
LENGTH: 1516
TYPE: DNA
ORGANISM: Homo sapiens NAME/KEY: unsure ESULT 2 S-09-974-298-92 121

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                                                                              1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500
1441 CATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTATGTAGCTG 1500
1381 TIAIAITAIAACICTGIATAATAGAGATAAGTCCATTTTTAAAAATGTTTTCCCCAAAC 1440
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99.9%; Score 1515; DB 14; Length 1516;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1516; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 1303785CB1
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SUBJECT STRUCK APPLICANT: SUBJECT STRUCK APPLICANT: Jed G. Nuchtern APPLICANT: Sharon E. Plon APPLICANT: Sharon E. Plon APPLICANT: Sharon B. Plon TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION FILE REPRENCE: PA-0046 US. CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR PILING DATE: 2001-02-23
NUMBER: OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; CTHER INFORMATION: a, t, c, g, or other US-10-084-817-8
                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10084817; Publication No. US20030119009A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                             1501 AAAATAAATGNCGTC 1516
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ORGANISM: Homo sapiens
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      241 GAAAATGAAGAGCAGGAATATGTTCAAACTGTGAAGTCATCCAAAGGTGGTCCCCGGATCA 300
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                                                                                                          March 10, 2004, 09:19:42; Search time 168.644 Seconds (without alignments) 12152.440 Million cell updates/sec
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

1. /cgn2_6/ptodata/2/ina/BE_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-576-15155
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US-09-817-180-1	US-10-003-295-1	US-10-204-708-72	US-08-487-826B-13	US-10-204-708-30	US-08-628-417-6	US-09-328-475C-50	US-09-252-991A-14965	US-09-252-991A-14667	US-09-252-991A-14785	US-09-443-041A-27	US-09-417-485D-5	US-09-621-976-2813	US-10-204-708-57	US-10-204-708-85	US-10-204-708-46	US-09-790-988-1	US-09-712-016-36
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ALIGNMENT

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APPLICANT: Furness, Michael
APPLICANT: Burness, Michael
APPLICANT: Burness, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARS: PERL PROGRAM
SSQ ID NO 908
LENGTH: 3693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 İGİTİTİLGIĞĞAĞÇĞĞĞÇĞĞĞATĞTĞTĞÇAÇTÇAÇAĞAĞAĞĞĞĞAAÇÇÇAÇÇTÇT 240
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100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels 0;
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; OTHER INFORMATION: Incyte ID No. 6673549 1505038CB1
US-09-976-594-908
          ; Sequence 908, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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US-09-976-594-908
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	Db 1561 TTTTGGGAGGGTACACCCAAATGATGGC Qy 1621 CTAACCAAATTTTAAAAAAACTTTTTACC Db 1621 CTAACCAAATTTTAAAATACTTTTTACC Qy 1681 TTTGGCAAGTTGACTTTATATTTTACCAATTTTTACC Db 1681 TTTGGCAAGTTGACTTTATTTCTTCAATT	1741 ATTTTCTTGACTAGGTATTA 	1921 IGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG		2341 2341 2401 2401 2461
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Sequence 15155, Application US/09621976
Patent No. 6639063
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Best Local Similarity 99.8%;
Matches 894; Conservative (
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Pred. No. 2.1e-243;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOBET, S.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: OS4PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12155
LENGTH: 896
                                                                                      3661 ATGAATAAAGAAATTAAAGTGAAAAAAAAAAAA 3693
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Sequence 540, App
Sequence 540, App
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Sequence 209, App
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Sequence 941, App
Sequence 617, App
Sequence 144, App
Sequence 3903, Ap
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Sequence 20, Appl
                                                                                                                           March 11, 2004, 03:37:21; Search time 860.54 Seconds (without alignments) 15799.545 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/prodata/1/pubpna/PCT_NBW PUBL seq:*

3: /cgn2_6/prodata/1/pubpna/DCG_NBW PUB seq:*

4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

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7: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Sequence 546, App
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Sequence 16944, A
Sequence 24844, A
Sequence 24844, A
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Sequence 209, App
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                                               US-10-085-7837-56883
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US-10-085-735A-56713
US-10-085-735A-56713
US-10-085-785-7857
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US-10-085-783A-42307
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                 US-09-738-973-546
US-09-854-133-546
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ALIGNMENTS

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APPLICANT: Kaser, Matthew R.

IIILE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REPERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION DATE: 2000-07-28
SPRIOR FILING DATE: 2000-07-28
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1505038CB1
US-09-919-039-359
                 ; Sequence 359, Application US/09919039; Publication No. US20030108871A1; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 3693; Conservative
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US-09-919-039-359
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Db 3421 ACTCTGGACTATATCAGTTTTTGGAAAGCAGGGTTCCTCTGCCTGC	RESULT 2 US-10-084-817-20 US-10-084-817-20 Sequence 20, Application US/10084817 Publication No. US20030119009A1 Publication No. US20030119009A1 General Information: APPLICANT: Susan Stuart APPLICANT: Sharon E. Plon APPLICANT: Sharon E. Plon APPLICANT: Abson M. Shohet TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION PILE REFERENCE: PA-0046 US CURRENT APPLICATION NUMBER: US/10/084,817 CURRENT FILING DATE: 2002-02-25 PRIOR PILING DATE: 2001-02-23 WUMBER OF SEQ. ID NOS: 365 PRIOR FILING DATE: 2001-02-23	SEQ IN NO. 2: LENGTH: 3693 LENGTH: 3693 TYPE: DNA ORGANISM: Homo sapiens PEATURE: NAME/KEY: misc feature OTHER INFORMATION: Incyte ID No. US20030119009A1 1505038CB1 US-10-084-817-20 Query Match Best Local Similarity 100.0%; Score 3693; DB 14; Length 3693; Matches 3693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CTGCCGCCGTCCTGCCCCGCCCCCCCCCCCCCCCCCCC	
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Sequence 3098, Ap
Sequence 8225, Ap
Sequence 110305,
Sequence 110306,
Sequence 317, App
Sequence 317, App
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Sequence 120, App
Sequence 23651, A
Sequence 16444, A
Sequence 11619, A
                                                                                                                                     March 11, 2004, 03:37:21 ; Search time 298.498 Seconds (without alignments) 15799.545 Million cell updates/sec
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                                                                                                                                                                                                                                                                                  Sequence 8
Sequence 3
Sequence 3
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1. cgm2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
2. cgm2-6/ptodata/1/pubpna/DS0_NEW PUB.seq:*
3. cgm2-6/ptodata/1/pubpna/US06_NEW PUB.seq:*
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7. cgm2-6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-102-806-120

US-09-18-995-136444

US-10-198-846-11619

US-10-198-846-11619

US-10-198-946-3098

US-10-198-946-3098

US-10-282-122A-25713

US-10-027-632-110305

US-10-027-632-110305

US-09-991-936-17

US-10-027-612-110305

US-10-104-644-831

US-10-1184-644-831
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Maximum Match 100%
Listing first 45 summaries
                                                                                             M nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 412, Ap
Sequence 4949, Ap
Sequence 1, Appli
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Sequence 574, App
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                                                                                                                                        sequence 412,
sequence 412,
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OTHER INFORMATION: Incyte ID No. US20030119009A1 1497123CB1
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APPLICANT: Jed G. Nuchtern

APPLICANT: Sharon B. Plon

APPLICANT: Sharon B. Plon

APPLICANT: Jed G. Nuchtern

APPLICANT: Sharon B. Plon

TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

FILE REPRENCE: PA.0046 US

CURRENT APPLICATION NUMBER: US/10/084,817

CURRENT FILING DATE: 2002-02-25

PRIOR PILING DATE: 2002-02-25

NUMBER OF SEQ ID NOS: 365

SOFTWARE: PERL PROGRAM
US-10-123-155-412

US-10-146-731-412

US-10-140-472-412

US-10-140-472-412

US-10-140-885-412

US-10-130-811-412

US-10-140-865-412

US-10-140-864-412

US-10-140-864-412

US-10-140-864-412

US-10-140-864-412

US-10-140-864-412

US-10-156-761-4949

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US-10-184-644-574

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US-10-142-885-204

US-10-13-15-204

US-10-13-15-204

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US-10-13-17-56-204

US-10-13-17-56-204
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US-10-140-805-204
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ORGANISM: Homo sapiens
    SEQ ID NO 1
LENGTH: 1281
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US-10-084-817-1
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ndels 1; Gaps 1;
CTCAGCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTC 1260
                                                                                                                                                                                                                                                                                                                                   CCCCATATCTGTTTGGAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCGCTGGGGAGAGAG 548
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                                                                                                                                                                                                                                                                                                    ACGAGGGGAGGCTGCTCT 68
                                                                                                                                                                                                                                                                                                               ACGAGGGAGGCTGCTCT 68
                                                                                                                                                                                                                                                                    Length 1308;
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CTTGTTCTGGGCAAGAACCCAAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1268
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                                                                                                                       609 ATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAAGGCCTAT 668
                                                                                                                                                                                                608 ATCTGGCTGGTGACTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGGAGGCCTAT 667
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                                          548 AAACGCCAGGCTGACCCAGGCCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCC 607
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23651, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1268 CAAAAAAAAAA 1280
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IS-09-918-995-23651
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ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature

SEQ ID NO 23651 LENGTH: 475

TYPE: DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CCTGTGCGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCC 393
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                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 394.2; DB 10; Length 407; 98.0%; Pred. No. 1.6e-107; tive 0; Mismatches 8; Indels 0;
                                                                                                             Query Match
31.1%; Score 398.6; DB 10; Length 475;
Best Local Similarity 97.8%; Pred. No. 7.9e-109;
Matches 404; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %30-918-995-16444, Application US/09918995

FORDILCALION NO. US/0030073623A1

GENERAL INFORMATION:

APPLICANT: Hyeaq, Inc.

TITLE OF INVENTION:

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TOTAL OF INVENTION:

TOTAL OF THE OFFICE ACID SEQUENCES OBTAINED

TITLE OF INVENTION:

TOTAL OF THE OFFICE ACID SEQUENCES OBTAINED
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SQFTWARE: PSECEO for Windows Version 3.0
// LOCATION: (1)...(475)
// OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23651
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                                                                                                         369 GACTICGIGACCGAGGCGCTGCAGAGCAGACTIGGAGCTGATGICTGIGCTGTCTCTCCGG 428
                                                                                                                                                                   241 GACTTCGTGACCGAGGCGCTGCAGACCAGACTTGGAGCTGATGTCTGTGCTGTCCTCCGG 300
                                                                                                                                                                                                                      429 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 488
309 CCGCTGGGAGGCGCCCCCGCGGCTGCTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 368
                                                                                                                                                                                                                                                                          301 CTCTCTGGTCCACTCAAGGAACAGTATGCTCATGAGCATGGCTTGAACTTCCAGAGACTC 360
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APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAGT CANCER
TITLE OF INVENTION: THERAPY OF BREAGT CANCER
TITLE OF INVENTION: THERAPY OF BREAGT CANCER
TITLE OF INVENTION: THERAPY OF BREAGT CANCER
TITLE OF INVENTION: WINDER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTRARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels 0; Gaps
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APPLICANT: Xu, Yongyao
APPLICANT: Xu, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 GCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGG 469
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                                                                                                                                                                                                                                                                                                                                         489 CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCG 535
                                                                                                                                                                                                                                                                                                                                                                                         361 crigoacaccadcaccracaagcacccrrrcccaaaccarcarcac 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11619, Application US/10198846; Publication No. US20030099974A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3098, Application US/10198846, Publication No. US20030099974A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1, 2, 3, 4
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 95.61
Matches 108; Conservative
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US-10-198-846-3098/c
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US-10-198-846-11619
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LENGTH: 469
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APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Elis
APPLICANT: WINTZ, Elis
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: PAIGLER, Simchon
TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REPRENCE: 36668-0005
CURRENT APPLICATION NUMBER: US 60/287, 724
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%; Score 76.4; DB 14; Length 906;
Best Local Similarity 76.8%; Pred. No. 1.9e-12;
Matches 119; Conservative 0; Mismatches 32; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1, 24, 346, 350, 495, 630, 632, 638, 640, 657, 663, 684,
LOCATION: 61, 711, 736, 755, 762, 766, 780, 817, 825, 826, 845,
LOCATION: 849, 864, 879, 881, 894, 897, 904, 905
OTHER INFORMATION: n = A,T,C or G
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CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 60; Conservative
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US-09-908-975-8225
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US-10-282-122A-25713
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                                                                                                                                                                             SEQ ID NO 3098
LENGTH: 906
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                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Frior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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Sequence 25713, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                           1859 CCGAGGAGGACCTCG 1873
                                                               APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Forsyth, R.
                                             GENERAL INFORMATION:
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LENGTH: 2100
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APPLICANT:
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                                                                                                                                                                       APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR PULLOATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-4
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRASESQ for Windows Version 4.0
SEC ID NO 110305
US-10-027-632-110305/c; Sequence 110302, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 TÁTCCGCAGGAACNCAGATÁTAAAATGGTTTATTGAAAATATGGTGCTAAAGTTTATAAC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 NATTAGAATTAATTGCAGTAAATGCATTCGANAATNTCGAGGTTGGAAATTTACNGAAGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 GGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGGACTTTGACTGGGTCAT 805
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                                                                                    559 GGAGGAGGGCTGGCAGAGGAGAAGGGCTGAGGAGGTACTGGAAAAGAAAAGAGAGGGGGG 500
                      765 GAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaines, Parrick J.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND WALPIGHIAN TUBULE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
FILE REFERENCE: FC-6-C1.
CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1090-04-09
NUMBER: OF SEQ ID NOS: 1959
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 AGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCCATCTGGCTGAGGTGA
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3.8%; Score 48.2; DB 10; Length 500;
Best Local Similarity 48.4%; Pred. No. 0.00045;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10271416
Publication No. US20040043021A1
GENERAL INFORMATION:
APPLICANT: Little, Randall D.
APPLICANT: Van Esrdewegh, Paul
APPLICANT: Dupuis, Josee
APPLICANT: Railen, Richard G.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: ALlen, Kristina
ITILE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
                                                                                                                                                              825 CAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGA 859
                                                                                                                                                                                                                             499 gagerggaggaagaacgregaggaggagga 465
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 317, Application US/09991936; Publication No. US20030073827A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brandt, Kevin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 CGAGAA 811
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LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               679 AAGGAGCAGGAGGAGGAGCTGGGGGAAGAGGAGGAGCTAAGAAAAAAAGGAGAGATG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705 GAGCAGAGCGAACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCA 764
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4.0%; Score 50.6; DB 15; Length 2057;
Best Local Similarity 40.0%; Pred. No. 0.00012;
Matches 206; Conservative 0; Mismatches 309; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10882-1.29
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                       499 GAGCTGGAGGAAGACGTGGAGGAGGAGCTGGAGGA 465
825 CAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-022-2
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR PLILNG DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                    ; Sequence 110306, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                  RESULT 10
US-10-027-632-110306/c
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LENGTH: 2057
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66 DKYGKPNYRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRGV 125
251 AAGCICTGGTTCCCCGACCGCCTCCACAGGACTACCTCGAGGTGATGTTCACCAACCGC 310
                                                                                                                                                                                     543 GAGGAGAAACGCCAGGCTGACCCCAGGCTTCTTTGCAGGAAGATTGTGGAGGGCATCTCC 602
                                                                                                                                                                                                                                           311 AAGGAGAGAGGCGAGCTGCTGGAAGGTTTGGTGGTCAGCAACAAAGACGCCCACCGTGCCC 370
                                                                                                                                                                                                                                                                                           603 CAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAG 662
                                                                                                                                                                                                                                                                                                                                              371 Grecrecceagaaaracrecrerreresesaaaaaacsacaacarerreacareses 430
                                                                                                                                                                                                                                                                                                                                                                                                    663 GCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGAGGAGCAGAGCGGCGACAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 CTCGCCAAGACAATGAAAGAGCAGCTCGGCGAGAAGACGACGCCTGCAGAGCATAAGCAAG 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 MAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597 ATCTCCCAGCCCATCTGGCTGGTGAGTGACACGGAGAGTGTCTGACATCCAGTGGTTT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 EBENSESSESEKTSDODFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 CGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGCAGAGCCGA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPRENCE: P3430RLC227 CURRENT APPLICATION NUMBER: US/10/184,644 CURRENT FILING DATE: 2002-06-28 Prior Application home of See File Wrapper or Palm NUMBER: OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 42.2; DB 14; Length 671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 CGGGCTGGGTGTT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 GCCGGCCACCTGGT 504
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Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTIONN: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTIONS: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21466 CCTGTGCCAGCGGGGATCTGCGGCTGATGTATGGCATGTGGGGCTGGAAAGCTGCCATCA 21525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21526 TAGCCCAGTAGCGGAAGGAAAACGGAGAGGTCCTGGCGGTGCTGGCCTGAGGCTCAGTG 21585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 GAGGCGCCCCCCCCCCCCCCCTCCTCTTCACCCCCCAAGAGGAAATCCCGGAAAGGACTTCC 375
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.7%; Score 47.4; DB 12; Length 22693; Best Local Similarity 53.5%; Pred. No. 0.0021; Matches 99; Conservative 0; Mismatches 86; Indels 0;
           RELATING TO RESPIRATORY DISEASES AND OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.4%; Score 43.6; DB 12; Length 830;
Best Local Similarity 43.8%; Pred. No. 0.012;
Matches 190; Conservative 0; Mismatches 244; Indels 0;
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; OTHER INFORMATION: Clone ID: 700093880_FLI
JS-10-425-114-831
                                                                               CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/328,424
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 22693
                               FILE REFERENCE: 2976-4045
CURRENT APPLICATION NUMBER: US/10/271,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 831, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
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           TITLE OF INVENTION:
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IS-10-425-114-831
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LENGTH: 830
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957 CGATCCTGGCCGAGGTGAGGAACAGAGGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGA 1016
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717 CAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTG 776
                                             306 DSDEVDRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERG 365
                                                                                                                                                   366 SGGSSGDELREDDEPVKKRGRKGRGRGPSSSDSEPBAELEREAKKSÅKKPQSSSTEPAR 425
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                                                                                                                                                                                                                                        897 AGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCCC 956
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                                                                                                      777 GACAACTICGGGGACTITGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAG 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3%; Score 42.2; DB 14; Length 671; Best Local Similarity 6.9%; Pred. No. 0.03; Matches 38; Conservative 202; Mismatches 305; Indels 2
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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US-10-184-634-346
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ENGTH: 671
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957 CGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGGTTGGTGGA 1016
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                                       306 DSDEVDRISEWKRRDEARRRELEARRREQEEELRRIREQEKEEKERRERADRGEAERG 365
                                                                                                                         366 SGGSSGDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPAR 425
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                                                                                        777 GACAACTICGGGGACTITGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAG 836
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717 CAGCAGCGGGGCTGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTG 776
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469 GCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-621-976-3203
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NAME/KEY: CDS
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Best Local S
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Sequence 14, Appli
Sequence 2, Appli
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16656, A
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41, Appl
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                                                                                                                                                            March 10, 2004, 09:19:42; Search time 58.4979 Seconds (without alignments) 12152.440 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/RECOMB.seq:*
/cgn2_6/ptodata/2/ina/RCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             M nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 5574, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 9594, Ap
Sequence 9701, Ap
Sequence 9701, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 10932, A
Sequence 10932, A
Sequence 11256, A
Sequence 11256, A
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      Sequence 327, App
Sequence 2, Appli
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Ratent No. 663063

GENERAL INFORMATION:
APPLICANT: Unbear Milne Edwards, J.B.
APPLICANT: Uobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REPRENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 3203
LENGTH: 419
                         3 US-09-103-840A-2

3 US-09-103-840A-1

US-09-103-840A-1

US-08-2489-3657-4

US-08-240-357-1

US-09-252-991A-9701

US-09-252-991A-960

US-09-252-991A-960

US-09-252-991A-11239

US-09-252-991A-14239

US-09-252-991A-14239

US-09-252-991A-14239

US-09-252-991A-14239

US-09-252-991A-14239

US-09-252-991A-14239

US-09-252-991A-140925

US-09-252-991A-140925
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US-09-252-991A-10995
   US-09-072-967-327
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      ; LOCATION: 75..380
US-09-621-976-3203
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589 IGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCC 648
                              649 AGIGGITICGGGAGGCCIAIGGGGCCGTGACGCAGACGGICCGCGTIGIAGCGTTGGAGC 708
                                                                                                                           355 AGTGGTTTCGGGAGGCCTATGGGG-CGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGC 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.8*; Score 1.7; LL.,
Best Local Similarity 3.3*; Pred. No. 0.002;
Matches 13; Conservative 218; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENI INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                               ; Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid.
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(703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: pTZgpt-F1s
US-08-232-463-14
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IMMEDIATE SOURCE:
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US-08-232-463-14/c
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121 GTTTGGACATGAGCTGAGGGCACGGTCGCGGCGGTCAGCCCTGTTCGCAGCTACGGCGA 180
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                                            771 GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
                                                                                                                                     831 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGT 890
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WHITE, Owen R.
APPLICANT: FASSER, Claire M.
APPLICANT: VENTER, JOHN
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REPERBENCE: 2436-22007.00
CURRENT REPERGUE: 1959-2007.00
CURRENT PILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  1011 GGTGGATATTGGGCAAGGCAGGAAACCTC 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; RAREAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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datches 127, Conservative
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Query Match
3.1%; Score 39.6; DB 4; Length 1665;
Best Local Similarity 49.1%; Pred. No. 0.41;
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps
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; Patent No. 6551795
; GENERAL INFORMATION:
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; Sequence 7242, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1536
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3.1%; Score 39.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 5.9;
Matches 127; Conservative 0; Mismatches 127; Indels 1; Gaps
                                                                                                                                                       APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 39.6; DB 4; Length 1536; 49.1%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SUPPRERE PEC ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: H37Rv
                                Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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Best Local Similarity
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US-09-252-991A-7459
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JS-09-103-840A-1/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREQGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AREQGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT PRICE REFERENCE: 107196.136 CURRENT PAPLICATION NUMBER: US/09/252,991A CURRENT PILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PAPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
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                                                                                307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGAAATCCGGGA 366
                                                                                                                                                       830 cccacacadacatacatacatricaracridatadacatricaracradacacacacaca 889
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0; Gaps
0; Mismatches 109; Indels
    Matches 105; Conservative
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RESULT 10
US-09-252-991A-6339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%; Score 39.6; DB 4; Length 1713; Best Local Similarity 49.1%; Pred. No. 0.41; Matches 105; Conservative 0; Mismatches 109; Indels 0;
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20.9%; Pred. No. 0.41;
tive 92; Mismatches 120; Indels 0
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TILLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION UNMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 7383 LENGTH: 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2574, Application US/09621976 Patent No. 6639063
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                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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Matches 56; Conservative
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US-09-621-976-2574
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US-09-621-976-2574/c
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Sequence (420, Application US/09252991A)

Sequence (420, Application US/09252991A)

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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97 MASWRSWSYMYMYWSSKYCASGWSKCAWSKGMTMCYYSKGYYTCRSMSYYKYSASYGSCW 38
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-07-27
NUMBER: OS SEQ ID NOS: 33142
                                                                 505 ACAAGGAGGCCTTTCGGAAGGACATGAT 532
                                                                                                    37 CCYGKSYCKSSMYAASSYCCSGSWWMMT 10
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Patent No. 6551795
GENERAL INFORMATION:
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Matches 82, Conservative
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                   0; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 304, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1998
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MEDIUM TYPE: Floppy disk
SOFTWARE: Microsoft Office 97 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                      Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CONNUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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OPERATING SYSTEM:
                                                                                                                                                                                                                Best Local Similarity
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                                                                                TYPE: DNA ORGANISM: Zea mays
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                                                                                                                                  US-09-647-224A-9
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                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2081 GEGIOGGCAACGICCCGGIGGGCGGCGACGCGCCGAICGCCGIGCAGGAGCAIGACCAACA 2022
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                                                                                                                                     355 GGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCT 414
     39 GGGTGGCAACGTCCCGGTGGGCGGCGACGACGGCGGTGGCATGACCA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Falco, Saverio Carl
APPLICANT: Falco, Saverio Carl
APPLICANT: Falco, Saverio Carl
APPLICANT: Falco, Saverio Carl
APPLICANT: Gutteridge, Steven
APPLICANT: Maxwell, Carl A.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rollmer, Steven J.
TITLE OF INVENTION: TRYPTOPHAN BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB-1150-A
CURRENT APPLICATION NUMBER: G0/079,386
FRICH APPLICATION NUMBER: G0/079,386
FRICH APPLICATION NUMBER: G0/079,386
FRICH APPLICATION NUMBER: PCI/US99/06046
FRICH STALING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 32
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                  15-09-252-991A-6131/c
; Sequence 6131, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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// Patent No. 6482631
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-07-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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938 GAGGGGGGAAGGGKWWNRAMMGGGGGRGTNKAGAKGGGGSGMGRGWAWSGMGGKWGGG 879
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                                                                                                                                                                                                                                                                     Query Match 2.9%; Score 37; DB 4; Length 1036; Best Local Similarity 29.3%; Pred. No. 1.7; Matches 118; Conservative 55; Mismatches 230; Indels
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMITITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Nero, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Print
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 309, Application US/09072967; Patent No. 6592877
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 304:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                              LENGTH: 1030 Date TYPE: nucleic acid
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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 37; DB 4; Length 1036;
29.3%; Pred. No. 1.7;
tive 55; Mismatches 230; Indels
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                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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RER: US 60/074,788
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILLIO BATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-252-991A-532/c
; Sequence 532, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                           TELEPHONE: (206) 622-4910
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                          LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-072-967-309
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LENGTH: 831
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U U O	9 CCGCGTTGTAGCGTTGGAGCAC	9 ccacricgrircgccgaracc	9 gapcangcnaagrcagaang

⁷⁴⁹ GGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTGGTGGGTCATGAG B08

229 GGAGCGGTTGCTTTACCGCTGTGCCGTGGACAACTTCTGGGAGCTGGACAGCGTCACGA 170

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⁸⁰⁹ GAACCATGGAGTTGAACAGGGC 830

¹⁶⁹ GCGCGAGGTGATCGGCCGGCAC 148

Search completed: March 11, 2004, 14:41:22 Job time : 76.4979 secs

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March 10, 2004, 08:01:57; Search time 311.77 Seconds (without alignments) 17454.974 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Listing first 45 summaries
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distribution.	Description	f21733 Human br	364	29232 Human a	t23873 Human ge	20639 Human	119 Оговорыі	11749 Human	30118 Drosop	30184 Drosop	35477 Human	71938 Rice g	51434	37843 Prokaryo	93822	3011	N	3426	142 Mycobact	ation (29	inuation (30	Continuation (29 o	0	
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ACA42257 ABA04108 ABA04112 AAZ17263	AB199884 ACA42498 AAZ22859 AAN71319	AAZ19421 AAZ19421 AAE98718 AAS94894 AAAS1616	ADA71938 AAAS1614 AAAS1615 AAL44550 ABL39955	ADB68842 AAI29394 ABZ33580 ACA56522
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ALIGNMENTS

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AABS8711 - AABS9128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                       Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nocotropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antilifammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyrodiditis; diabetees mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                        Human breast and ovarian cancer associated antigen gene SEQ ID 120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 571; 1299pp; English.
                                 AAF21733 standard; DNA; 1308 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999; 99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                     WO200055173-A1.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                       27-MAR-2001
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                                                                  AAF21733;
RESULT 1
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isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit optostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatoxy; antiulcer; vulnerary; anticonvulsant; antibacterial; antiinflammatoxy; antioler; vulnerary; anticonvulsant; antibacterial; antiinflammatoxy; antipacatic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crobn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
sequences AAF22032 - AAF22040 and AAB59129 which are used in the
                                                                                                                                                                                                                                                                                                                                                                            infectious diseases
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Sequence 1308 BP; 280 A; 325 C; 433 G; 269 T; 0 U; 1 Other;

ä 728 247 548 547 608 607 668 667 788 248 GACTICGIGACCGAGGCGCIGCAGAGCAGACTIGGAGCIGAIGICIGIGCIGICCICCCGG 428 CTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGACTC 488 487 668 gagaccárakcackakcarccacarrarkacarragkackadakaccakackackáckáckáckácká GIGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATATCTGTTTGGAC 128 TITTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATGGCGAGGCGTGGCGGCCCCATGGCC 308 CCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGGAAATCCGGGAAG 368 ccecreseasecccccccccccresracrecrerreacecccaasaaarccecaas GACTICGIGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGICTGTGCTGTCCTCCGG 427 Greandeancedecrificierecedesteretecetrificieedeanniciditificade 128 129 Arcadcraadedcaccaccicccedededercad-cordricecadoraccaccaageagege 187 rrrradederadedadaderercaderricadecardedededededededededededed 307 68 68 548 AAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGCCC 609 ATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCTAT TGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGGCCTGGACAACTTCGGG CTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGAAG 608 Arcrescricereacreacacacacada a deferencia carceacacacacada de contra GGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCGACAGCGGGGGC ATGAGCTGAGGCCACGGTCGCGGCGCGCTCAGCCCTGTTCGCAGCTACGGCGAAGAGGGGC GCGATTGYTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGCGCTCCATTCCGCGCGGCGTGTCCCGA CGGGGCTGGACTCTAAGTGAGTTCGGGTGGGGGGGCTTCACGAGGGGAGGCTGCTCT cacarccaacraricinaagraagricaagricaagaagciircacaagaagaagacraci 1; Gaps Score 1255.8; DB 3; Length 1308; Pred. No. 0; 3; Indels 1; Mismatches 98.0%; Best Local Similarity 99.6 Matches 1268; Conservative 549 699 729 489 249 368 428 248 309 308 369 429 g g ò 셤 ò

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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

1089 AGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATC 1148 1088 AGACTCCAAGGCCAAAGGAGGGTGTCTTGGCTTGAAGGCGAAACCCTGCCATATC 1147 1149 CCCAGTGCCCAGTCCCCTCAGCCTGTGGTGGCTTGCATCCTGACTGGATGTTCTCAGCCC 1208 1148 cccharaccharaccranaccranagrascringchracharacharacranarrachaga 1207 1209 CTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCA 1268 1208 CITGITCIGGGCAAGAACCCAGAGCTCCCCAGIGIGGAIACIAAIAAACCICITGGAGCA 1267 1028 968 Aggraagaacagacagagagagarcragarricraagagagrragragaararragacaagg 1027 CAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGG 1088 1028 caddaaaccrcrigaadaccrcarrrrcrccardgaaaaacaacaadcrcrrcragaagg 1087 967 907 CCTGCTGAGGTGGGGGTGAGTGTCTGCAAAATGGGGGTGTCCCCCGATCCTGGCCG 968 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG 908 789 GACTITGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAG 848 Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. 728 TGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGG 787 848 AACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGG ccrecreaedededededecreaecreaedaaaarededederereceedarecerededede 969 AGGTGAGGAACAGACAGGGGGGGTCTAGATTCTGAGGGGG Giordano J; Human secreted protein 5' EST, SEQ ID NO: 2133. Duclert A, 21-FEB-2000; 2000EP-00200610. AAC02135 standard; cDNA; 465 99US-0122487P 1269 CAAAAAAAAAAA 1281 1268 CAAAAAAAAAAA 1280 06-OCT-2000 (first entry) Dumas Milne Edwards J, WPI; 2000-500381/45. P-PSDB; AAG02129. (GEST) GENSET EP1033401-A2. 26-FEB-1999; Homo sapiens. 06-SEP-2000. 849 606 908 RESULT g ò 음 ò a ò 원 ò 요 ઠે 셤 ਨੇ 음 ò 셤 ò d ठ

17-APR-2003.

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The present sequence is one of a large number of 5' ESTs derived from manyas encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length company sequences where the sequences to be sed to obtain full length gene therapy and chromosome mapping procedures. They are used to obtain upper ream regulatory sequences and to design expression and secretion
Claim 1; SEQ ID NO 2133; 71pp + Sequence Listing; English.
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Sequence 465 BP; 92 A; 117 C; 160 G; 90 T; 0 U; 6 Other;

vectors

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247 GATTTTAGGGGTAGGGAGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 306
                                                                                                                                                                                                                                                                                                                         CCCCGCTGGGAGGCGCCCCGCGGGTGGTACTGCTGTTCAGCGRCAAGAGGGAAATCCGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAAGGCCT 666
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                                                                                                                                                                                                              1 GATTTTAGGGGTAGGGAGAÁGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 60
                                                                         0; Gaps
Query Match 35.8%; Score 459.2; DB 3; Length 465; Best Local Similarity 98.5%; Pred. No. 6.2e-117; Matches 458; Conservative 3; Mismatches 4; Indels 0;
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Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                    Human endothelial cell cDNA #4572.
                   ACH36439 standard; cDNA; 475 BP
                                                                13-OCT-2003 (first entry)
                                                                                                                                                               US2003073623-A1
                                                                                                                                           Homo sapiens.
RESULT 3
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polymetic comprising a sequence corresponding to a reading frame of the novel polymucleotide. The mucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for clearifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence for the this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       989 GGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCT 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 398.6; DB 8; Length 475;
Pred. No. 4e-100;
0; Mismatches 9; Indels 0;
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                                                                                                                                                                                                                                                               Drmanac RT, Labat I, Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 23651; 44pp; English.
                                        30-JUL-2001; 2001US-00918995.
                                                                                  30-JUL-2001; 2001US-00918995.
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Best Local Similarity 97.8%;
Matches 404; Conservative
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STACHE-CRAIN B.
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                                                                                                                             DRMANAC R T.
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                                                                                                                                                                                                               (JONE/) JONES L W.
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Human gene signature HUMGS05801. 94WO-JP001916. 93JP-00355504. 16-AUG-1996 (first entry) WPI; 1995-206931/27. MATS/) MATSUBARA K. (OKUB/) OKUBO K. WO9514772-A1. 12-NOV-1993; Matsubara K, Homo sapiens. 11-NOV-1994; 01-JUN-1995. AAT23873; 369 RESULT 5 AAT23873 셤 ઠે 엄 à g ò g $\stackrel{>}{\circ}$ g The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Mybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The mucleotide sequences are also useful as hybridisation probles, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is useful and to the 18043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formations. 189 GCGAITGTICCTIGTIGCCGCICCGCTIAGTGGCCGCGCCCATCCGCGCGGGTGICCCGA 248 129 ATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGGGC 188 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating Human, ss; sequencing by hybridisation, SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder. 0; Gaps Jones LW; DB 8; Length 407; 8; Indels Sequence 407 BP; 70 A; 120 C; 139 G; 78 T; 0 U; 0 Other; Drmanac RT, Labat I, Stache-Crain B, Dickson MC, segdata.uspto.gov/seguence.html?DocID=20030073623 30.8%; Score 394.2; DB 8 Similarity 98.0%; Pred. No. 6.2e-99; Conservative 0; Mismatches 8 Claim 1; SEQ ID NO 16444; 44pp; English. ACH29232 standard; cDNA; 407 BP 30-JUL-2001; 2001US-00918995. Human adult spleen cDNA #251. 30-JUL-2001; 2001US-00918995 13-OCT-2003 (first entry) STACHE-CRAIN B. DICKSON M C. JONES L W. antisense DNA or RNA. DRMANAC R T. LABAT I. WPI; 2003-615964/58. JS2003073623-A1. Homo sapiens. 17-APR-2003. Matches 399;

(STAC/) (DICK/) (JONE/) LABA/)

Query Match

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in ART19001-T26837 and which is able to hyporidise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (sep. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell
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afflicted with breast cancer by examining the correlation between the
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                                                                                                                                                                                                                                                                                             GITCICAGCCCCTIGITCTGGGCAAGAACCCAGAGCTCCCCAGIGGGATACTAATAAAC 1257
                                                                                                                                               1018 ATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCCATGGGGAAGACAGCCATGC 1077
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                                                                                                                                                                                                                                                                                                                      241 GIICICAGCCCNITGIICIGGGCAAGAACCCAGAGCICCCCAGINIGGAIACTIAITAAA 300
                                                                                                                                                                       61 ATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTTCTCCATGGGAAGACAGCCATGC 120
                                                                                                                        1 GATCCTGGCCGAGGTGAGGAACAGGGGGGGGTCTAGATTCTAAGGGGGTTGGAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is
                                                                         Gaps
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                                                                         0
                                                DB 2; Length 337;
                                                22.8%; Score 292.6; DB 2; Length: 92.9%; Pred. No. 8.4e-71; tive 0; Mismatches 23; Indels
                          Sequence 337 BP; 82 A; 76 C; 94 G; 72 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cancer expressed polynucleotide 13096.
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 function or for recognising different cell types
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL20639 standard; cDNA; 502 BP.
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24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
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                                                             Best Local Similarity 92.93
Matches 301, Conservative
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expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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                                                                                                                                                                                                                                                                                                                                                 Length 502;
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                                                                                                                                                                                                                                                                        Sequence 502 BP; 131 A; 148 C; 134 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          9.8%; Score 125; DB 4; Length 50: 96.2%; Pred. No. 2.9e-24; Live 0; Mismatches 5; Indels
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11-JUL-2000; 2000US-00614150
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nes 128; Conservative
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ABL30118/c
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                                                                                                                                                                                  337 TGCTGTTCAGCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGGAA 396
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                                                                                                                                                                                                                                                                                                                                       74 GATIGGGCTCCCGGTCGIGIA -- ICGITCGAAICTCAGAGCCCAITAAGTCGGAAIGGG 130
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                                                                                                                                                                                                                                  14 TACTCATCAGGGGCAAGCGAAAGTGCGGCAAGGATTACATATCCGAGAGGCTGCAGCGGA 73
                                                                   / Match 6.4%; Score 82; DB 4; Length 570; Local Similarity 51.9%; Pred. No. 2.6e-12; Los 268; Conservative 0; Mismatches 230; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 TICGGAAGGACATGATCCGCTGGGGAGAGAGAAACGCCAGGCTGACCCAGGCTTCTTT
                      Sequence 570 BP; 127 A; 148 C; 184 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cancer expressed polynucleotide 4206,
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24-MAR-2000; 2000US-0192099P.
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15-MAY-2000; 2000US-0205230P.
09-UTU-2000; 2000US-021315P.
25-JUL-2000; 2000US-02534P.
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319 GCGCCCCGCGGCTGCTGCTGCTTCAGCGCAAGAGGAAATCCGGGAA--GGACTTCGT 376
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                                                                                                                                                                                                                                                                       The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polymeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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                                                                                                                                       New peptide useful as a marker for the diagnosis of breast cancer.
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Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                       Claim 1; Page 767; 3695pp; English.
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11-JUL-2000; 2000US-00614150.
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                                                                   WPI; 2001-451856/48.
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Best Local Similarity
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1178 recagaaacecegrerecacedesaresaceriracecaesaarasacearearene 1119
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             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137-ABS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                        419 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGGATGGCTTGAACTT 478
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                                                                                                                                                                                                                                                                                                                                                                                         15; Gaps
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                                                                                                                                                                                                                                                                                                                                        Score 60.8; DB 4; Length 2673;
Pred. No. 3.7e-06;
0; Mismatches 202; Indels 15
                                                                                                                                                                                                                                                                                            Sequence 2673 BP; 610 A; 738 C; 638 G; 687 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3089 GAGCGÁCGÁGGAGCCGAGGACTACGGCTACTÍCTGCCGCGTGGCCATGGÁGGAGGC 3030
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                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidates, therappeutics and pharmaceutical fruge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-BB17017). The sequence data for this pærent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2909 TCCAGAAACGCGGTCTGCACGGGGATGGACCTTTACCGCAGGAATAGACGATGTTCCCTC 2850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2849 cdagrecearcrecarcarcresceaceacearcerecarerrescereceareareaceaes 2790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 CCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 GGGAGAGAGAAACGCCAGGCTGACCCAGGCTTCTTTGCAGGAAGATTGTGGAGG---- 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 -----GCATCTCCCAGCCCATCTGGCTGGTGACACACGGAGAGTGTCTGACAT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 CCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707 GC---AGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 AGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGA 823
                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 TGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 4.7%; Score 60.8; DB 4; Length 3406; Local Similarity 50.0%; Pred. No. 4.1e-06; nes 217; Conservative 0; Mismatches 202; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3406 BP; 965 A; 833 C; 729 G; 879 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 42025; 21pp + Sequence Listing; English.
                                                                                                     Myers EW
                                                                                                     Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN35477 standard; DNA; 60 BP
11-JUL-2000; 2000US-00614150
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                                                                                                     Venter JC, Adams M,
                                                                                                                                                       WPI; 2001-656860/75
                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                               interactions.
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The present invention describes oligonuclectide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several coligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries may also be used as specialised minicatering RNA transcripts of a sub-transcriptome under a particular colibraries to detect transcripts of a sub-transcriptome under a particular colibraries to detect transcripts of a sub-transcriptome under a particular colibraries to adetect transcripts of a sub-transcriptome under a particular colipogical or pathological state, and so allowing the detection of tissue colipraries to a specific genes such as those genes only expressed in colipogical transcriptome of a patient suffering from a particular collibraries of a transcriptome of a patient suffering from a particular collibraries of a transcriptome of a patient suffering from a particular collibraries of a patient suffering from a particular collibraries of a patient suffering from a particular collibraries of a patient suffering from a particular collibraries collibraries of a patient suffering from a particular collibraries pacefiles equences from crats, humans and mice, which are used in the exemplification of the printined specification, but was obtained in a lettorial format of direct of the printined specification, but was obtained in a secure of directed format of direction of the print of the printined specification, but whish with and middle of the printined specification, but whish with and middle of the printined specification, but whish with and the exemption of the printined s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-
                        Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wasserman A, Mintz E, Mintz L, Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60 BP; 13 A; 17 C; 15 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Fred. No. 1.3e
Matches 60; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                 20-JUL-2001; 2001WO-IB001903.
                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                      (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific genes.
                                                                                                                                                                   WO200210449-A2.
                                                                                                                Homo sapiens.
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1194 GGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 1253 0; Gaps 0; Indels Score 60; DB 6; Le Pred. No. 1,3e-06;

Length 60;

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1 GGATGTTCTCAGCCCCTTGTTCTGGCAAGAACCCAGAGCTCCCCAGTGTGGATACTAAT 60

ADA71938 standard; DNA; 2000 BP. 20-NOV-2003 (first entry) Rice gene, SEQ ID 5263.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention. Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant Plant; bacterial infection; fungal infection; viral infection; rice; Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other; Glazebrook J, Goff SA, Ho Whitham S, Xie Z, Zhu T, Claim 27; SEQ ID NO 5263; 899pp; English. (SYGN) SYNGENTA PARTICIPATIONS AG Cooper B, 22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105. Chen W, Co. F, Quan S, WPI; 2003-175290/17. gene expression. WO2003000898-A1. Oryza sativa. Chang H, Ch Katagiri F, 03-JAN-2003 gene; ds

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241 TTSYSWACSSYTWCRSKRRSWAWNOWRKWRNSRSYGWYSWSYKOWMCTAYKKKSYYSRWCY 300 586 ITGTGGAGGGCATCTCCCAGCCCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACA 645 646 TCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGG 705 361 YMRWRWATERRRWAKKSSRISHRKKKKKKOMRKRKYKRMRGYSRMRSCKRARWKRCRS 420 286 CGAGGCGTGGCGCCCCCTTGGCCCCCGCTGGTACTGCTACTGCTTCA 345 346 GCGGCAAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAG 405 406 CTGATGTCTGTGCTGTCCTCCTGGTCCACTCAAGGAACAGTATGCTCAGGAGC 465 466 ATGGCTTGAACTTCCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGG 525 526 ACATGATCCGCTGGGGAGAGAGAAAGGCCAGGCTGACCAGGCTTCTTTGCAGGAAGA 585 706 AGCAGAGCCGACAGCAGCGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAG 765 121 RCARSGRMAGGSGRMMGGKSRMSYWMWCYARGCGSCKRKKSKGGSWGKTCRRGARGGSGW 180 0; Gaps 'Match 4.6%; Score 59.4; DB 7; Length 2000; Local Similarity 9.1%; Pred. No. 8.1e-06; Conservative 325; Mismatches 336; Indels 0; Query Match latches

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661 MKSTCTWMYYMSKYTYAKYGSYMRYRYRYRAWCMYMWRWYYRYRSYMTYMAWYTSSTRMAM 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxic effect, gene expression profile, hepatotoxicity, diagnostic marker, toxicity marker; toxicity progression; drug screening, primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining if a compound induces a toxic effect on a tissue or cell, for
                                                                                          766 AATGTGGCCTGGACACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAAC 825
                                                                                                                                                   826 AGCGCCTGGAGGAGCAGTTGGAGAAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCAC 885
                                                                                                                                                                                                                                    886 TAGGTICTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATG 945
                                                                                                                                                                                                                                                                             601 MCKRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGS 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1976.
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                                                                                                                                                                                                                                                                                                                                                                                                         1006 GGGTTGG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                  721 TGMKYSG 727
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Elashoff M;
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                                                                                                                The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises the preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       816 GGAGTIGAACAGCGCCTGGAGGAGCAGTIGGAGAACCTGATAGAATTTATCCGCTCCAGA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 egagargaacagreccreeaegarcaerreeaeaaccrrcreeaarrrrarrcareccaaa 408
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identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        876 CITIAGICACIAGGITCIAGGAGIGAGCIGGGGCCIGCIGAGGIGGGGGGGGGCTGACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56.8; DB 9; Length 467;
Pred. No. 2.3e-05;
0; Mismatches 92; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 467 BP; 99 A; 138 C; 93 G; 137 T; 0 U; 0 Other;
                                                                                   Claim 44; SEQ ID NO 1976; 874pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 996 GATTCTGAGGGGGTTGGTGGATAT 1019
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-0362899P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4%;
Local Similarity 54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            design; gene
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AAC93822 standard; cDNA; 500 BP.

Zyskind JW; Xu HH;

19-FEB-2001 (first entry)

us-10-084-817-1.rng

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleac acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a prometer operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated collypeptide for the fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity spainst a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which the test compound that inhibits proliferation of an oraganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of the strains is present in a culture or collection of strains, or in an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids are useful and a cellular proliferation of an expension of the canded and organism of the condense acids accenting and describing and an organism or the condense acids accention of the cellular proliferation of an expension of the condense accellular proliferation of an organism or for screening for homologous nucleic acids required for cellular proliferation of for screening the candidate molecules for acquired for cellular proliferation of for screening or candidate molecules for acquired for a candidate molecules for acquired for a candidate molecules for acquired for a candidate molecules for acq New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. drug discovery programs, or for screening homologous nucleic acids creeding discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences Malone C, Haselbeck R, Ohlsen KL, Carr GJ, Yamamoto R, Forsyth RA, Claim 14; SEQ ID NO 25713; 1766pp; English. Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU33973

Sequence 2100 BP; 364 A; 732 C; 719 G; 285 T; 0 U; 0 Other;

1739 regeccescarcrecarradeces de descripto de contracar d 1799 ATGTGTCGGCCCGGCACGTGGTGCAGCGGCTGCTGGCCGAGCTCGGCGGCATCGACCAGG 1858 1620 Girceccaagaagcegceceaagaggcccregaegcceecaagaaggcgargececearg 1680 gerececcecececeacrrecerrecacececrrecrearececarice readecece 121 GITIGGACATGAGCTGAGGGCACGGTCGCGGGCGGTCAGCCTGTTCGCAGCTACGGCGA 180 181 GGAGGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCATTCCGCGCGG 240 241 TGTCCCGATTTTAGGGGTAGGGAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCC 300 301 CCATGGCCCCGCTGGGAGGCGCCCCGCGGGCTGCTGCTGCTCAGCGGCCAAGAGAAT 360 1; Gaps Query Match
4.0%; Score 51; DB 7; Length 2100;
Best Local Similarity 52.5%; Pred. No. 0.0018;
Matches 134; Conservative 0; Mismatches 120; Indels 1859 CCGAGGAGGACCTCG 1873 361 CCGGGAAGGACTTCG 375 ò qq ò 셤 ò d ò g ઠે

RESULT 15 AAC93822/c

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The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HWT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention also relates to the canceded proteins. The invention, recombinant cells comprising the consistencies, and the proteins, and recombinant production of the proteins, antichodies against the proteins, amethod of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, rearment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used an infestations of example, the nucleic acids may be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acids and quantitate the presence of cat flea or other homologous nucleic acids and quantitate the presence of cat flea or other homologous nucleic acids and antiphodies, and in assays to identify modulators (agonists and entiphodies, and in assays to identify modulators (agonists and entiphodies, and in assays to identify modulators (agonists and entiphodies and antagonists may also be used as antiphodies and antagonists may also be used to survivity. The anti-hWT-HWT protein antibodies and antagonists may also be used to survivity. The antiphodies and antagonists and antiphodies, and in assays to identify modulators (agonists and content antibodies may also be used immunosophists may also be used to survivity. The antiphodies in samples (e.g., by enzyme linked immunosobhet assay (ELISA)). The present sequence represents a cat flea hyperbole and the invention
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                                                                                                                                                                                                                                                                                                                   Cat flea, hindgut and Malpighian tubule nucleic acid; HMT;
flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
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                                                                                                                                                                                                                                    Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:317.
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3.8%; Score 48.8; DB 3; Length 500;
Best Local Similarity 48.4%; Pred. No. 0.0039;
Matches 119; Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 126; Indels Conservative 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 1; Mismatches 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ctenocephalides felis.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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781 ACTICGGGACTITGACTGGGTCATCGAGAACCATGGAGTTGAACAGGGCCTGGAGGG 840
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llarity 99.5%; Pred. No. 1.2e-304;
Conservative 0; Mismatches 6;
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Matches 1275;
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Genome Sequence Centre,
cDNA Sequencing by: Genome Sequence Centre,
conforce Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
steven Jones, Jennifer Asano, Ian Bosder, Yaron Butterfield,
Susama chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Susama chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
susama chan, Readman Chiu, Chris Fjell, Erin Garland, Rob.
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeeven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I.; Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bossak, S.A., McBwan, P.J., McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodesgren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.E., Jones, S.J. and Marra, M.A., Length M. M. Man, M. Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 18 Row: £ Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127505. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Submitted (02-APR-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab.hoste="DH.0B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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/db_xref="LocusID:10654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help deek
Email: cgpbs.remail.nih.gov
Tissue Produrement: ACC
cDNA Library Preparation: Rubin Laboratory
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/db_xref="GI:13543887"
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/db_xref="taxon:9606"
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PUBMED
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721 AGCGGGGCTGGGTGTTCACGCCAGGGGTGATGATGAGAATGTGAGAATGTGGACA 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               665 Addictratidaddcidtidacdcadacddricdcdrifdradcdrifddadchdadccdacadc 724
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GPLKEQYAQEHGLNFQRLLDTSTYKEAFRKDMIRWGEEKRQADPGFFCRKIVEGISQP
                           IMIVSDTRÄVSDIGWĒREAVGAVTQTVRVVALEQSRQQRGŴVFTPGVDDAESECGLDN
FGDFDWVIENHGVEQRLEEQLENLIEFIRSRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCTGCTCTGTGAAGGAACCGCCTTTCTCTCCGCGTGTCTCACCCTTTTCTCCCCATAICT 120
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/note=="p-mevalo kinase; Region: Phosphomevalonate kinase.
Phosphomevalonate kinase (EC:2.7.4.2) catalyses the
phosphomevalonate into
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Direct Submission
Submitted (11-MAY-2001) National Institutes of Health, Mammalian
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/protein id="AAH07694.1"
/prof="G" | 11.14043403"
/db_xref="G" | LoousID: 10654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young, A., Zhang, L.-H. and Green, E.D.
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whilting, M., Madan, A., Rodrigues, S.,
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Homo sapiens phosphomevalonate kinase, mRNA (cDNA clone MGC:11362
IMAGE:3954909), complete cds.
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                                                        841 AGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACAAGGTTCTAGGAGTG 900
                                                                                                                                                                                                                      964
                                                                                         845 AGTIGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTG 904
785 ACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGC 844
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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5-diphosphomevalonate, an essential step in isoprenoid biosynthesis via the mevalonate pathway. This family represents the animal type of the enzyme. The other is the BRGs type, found in plants and fungi, and some bacteria (see pfam0028) /db_xref="CDD:pfam04275"
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Location/Qualifiers
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GPLKEQYAQEHGLNFQRLLDTSTYKEAFRKDMIRWGEEKRQADPGFFCRKIVEGISQP
IWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVDDAESECGLDN
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Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Agele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14043402.
Onchact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC).
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'db_xref="LocusID:10654"

'db_xref="MIM:607622"
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/clone lib="NIH MGC_20"
/lab_host="DH10B-R"
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OY 1207 CCCTTGG DD 1141 CCCTTGG CY 1267 CACAAA DD 1201 CACAAAA RESULT 3 HUMPHKI LOCUS LOCUS LOCUS DEFINITION HOMO SAD ACCESSION L77213.1 VERSION L77213.1 KEYWORDS CHOLESTE SOURCE NAMBSON CHOLESTE REFERENCE MAMMSIIS REFERENCE AUTHORS CHAMDIS RATTORS CHAMDIS CHAMDIS RATTORS CHAMDIS C	FEATURES SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE	mrna s'utr cds	misc_feature 3.UTR polyA_signal polyA_site	Query Match Best Local Similar Matches 984; Con Qy 286 CGAGGC Db 19 CGAGGC Qy 346 GCGGCA Qy 346 GCGGCA Qy 406 CTGATC
127 ACATGAGCTGAGGGCACGGCGGCGGTCAGCCCTGTTCGCAGCTACGGCGAGGAGGG 186 6 1 ACATGAGCTGAGGGCACGGTCGCGGGCGGTCACGCGAGGAGGG 120 187 GCGCGATTGTTGCTGGTGCGGGTCAGGCCGGTTCGCGAGCTACGGCGAGGAGGG 120 120 GCGCGATTGTTCCTTGTTGCCGGTCAGGCCGGTCCATTCCGCGGCGGTGTCC 180 121 GGCGATTGTTCCTTGTTGCCGCTCAGGTCGCGGTCCATTCCGCGGGGTGTCC 180 122 GCGCGATTGTTCCTTGTTGCCGGTCGGTTAGGGCGGTCCATTCCGCGGGGGTGTCC 180 124 GATTTAGGGGTAGGGAGAAGTGTCAGGTTCGCGGGGGCGGGGGGGG	487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 546	667 ATGGGGCCGTGACGCACGCCTCGCGTTGTAGCGTTGGAGCCGACAGCGGGG 726 1	847 AGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGG 906 181	CGAGGTGAGGAACAGAGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAA 960 GGCAGGAAACACTGGAGGGGGGTCTAGATTCTGAGGGGGGTTGGTGGATATTGGGCAA 960 GGCAGGAAACCTCTGGAGACCTCATTTCTCCATGGGGAGAGAGCGCTGTCTTCAGGA 108: GGCAGGAAACTTCTGGAGACCTCATTTTCTCCATGGGGAAACCTTGAGGAACCTTCAGGA 114: GGAGACTCCAAGGGCAAAGGAGGTGTTTTGGCTTGAGGCGAAACCCTGCCATA 116:
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/translation="MAPLGGAPRLYLLFSGKRKSGKDFYTEALQSRLGADVCAVLRLS
GPLKEGYAQEHGLNPGRLLDTSTYKEAFRKDMIRWGEEKRQADPGFFCRKIVEGISQP
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FGDFDWVIENHGVEQRLEEQLENLIEFIRSRL"
1002 bp mRNA linear PRI 24-JUL-1996 piens phosphomevalonate kinase mRNA, complete cds.
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/evidence=experimental
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/db_xref="taxon:9606"
/tisue type="liver"
/clone_lib="Stratagene"
/dev_stage="adult"
/note="(vector lambda_ZAPII)"
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                                                                                                                                                                                                                                                                                     379 TCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGG 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 AGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCAC 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     886 TAGGTICTAGGAGTGAGCTGGGGCCTGCTGAGGTGGGGGTGGGGCTGACTCTGCAAAATG 945
139 CTGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGC 198
                                             466 ATGGCTTGAACTTCCAGAGACTCCTGGACACCAGACACCTACAAGGAGGCCTTTCGGAAGG 525
                                                                                         199 ATGGCTTGAACTTCCAGAGACTCCTGGACACCCAGCACCTACAAGGAGGCCTTTCGGAAGG 258
                                                                                                                                         526 ACATGATCCGCTGGGGAGAGGAGAACGCCAGGCTGACCCCAGGCTTCTTTTGCAGGAAGA 585
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                                                                                                                                                                               259 ACATGATCCGCTGGGGGGGGGAGAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGA
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                                                                                                                                                                                                                                                             Suzuki, O., Sagaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
                                           linear
                                                       Homo sapiens cDNA FLJ26724 fis, clone PNC05489.
AK130234
                                                                                                                          oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
                                           mRNA
                                           1178 bp
                                                                                                            AK130234.1 GI:34526995
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AK130234

RESULT 4 AK130234

DEFINITION ACCESSION

ORGANISM VERSION KEYWORDS

SOURCE

REFERENCE

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Submitted (31-70-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-6639, Japan Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-6639, Japan Fax:81-3-5449-5286,

Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of Research Association for Biotechnology (RAB); cDNA library construction and 5'-and one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-and one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Rataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S., Terashima,Y., Matanbb,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Ofeuki,T., Sato,H., Nishikawa,T., Sugiyama,T., Irie,R., Nishikawa,T., Sugiyama,A., Kawakami,B., NBDO, human cDNA sequencing project
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/clone_lib="PNC"
/note="cloning_vector: pME18SFL3"
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/db_xref="taxon:9606"
/clone="PNC05489"
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Location/Qualifiers
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Park, J., Rolfs, A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., Labaer,J., and Brizuela,L.

Labaer,T., and Brizuela,L.

Direct Submitssion

Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.

Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and Hindill sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and Defore 'ATG' to provide Kozak consensus sequence: 'GG' after last codon and before Hindill site to maintain
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IWLVSDTRRVSDIQWFREAYGAVTQTVRVVALEQSRQQRGWVFTPGVDDAESECGLDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
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db_xref="GI:33303795"
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/evidence=experimental
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/protein_id="A445091.1"
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EQSRQQRGWVFTPGVDDAESECGLDNPGDFDWVIENHGVBQRLEBQLENLIBFIRSRL
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                          421 CGGGGCTGGGTGTTCACGCCAGGGGTGGATGCTGAGTCAGAATGTGGCCTGGACAAC 480
                                                                                                                               481 TTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAG 540
                                                                                                                                                                                                                                                                                                                                        Homo sapiens phosphomevalonate kinase (HUMPMKI) gene, partial cds. AF026069
723 CGGGGCTGGGTGTTCACGCCAGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAAC 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chambliss, K.L. and Gibson, K.M.
Direct Submission
Submitted (19-SEP-1997) Institute of Metabolic Disease, Baylor University Medical Center, 3812 Elm St., Dallas, TX 75226, USA Chambliss, K.L.
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/gene="HUMPMKI"
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| product="0.131, 3965,6507. .6636,7717. .7853|
| gene="HUMPMXI"
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Olivier, L.M., Chambliss, K.L., Gibson, K.M. and Krisans, S.K. Characterization of phosphomevalonate kinase: chromosomal localization, regulation, and subcellular targeting J. Lipid Res. 40 (4), 672-679 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence update by submitter
On Sep 25, 1998 this sequence version replaced gi:3445541.
Location/Qualifiers
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Query Match
41.2%; Score 528; DB 9; Length 8862;
Best Local Similarity 100.0%; Pred. No. 4e-120;
Matches 528; Conservative 0; Mismatches 0; Indels C

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Fragment Name Begin End
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AL672265_3
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Continuation (2 of 6) of AL672265 from base 100001 (AL672265 Homo sapiens chromosome 1 c
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                                               7715 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGGT 7774
                                                                                                                                                                                                                                           7835 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGGCCTGCTGAGGTGGG 7894
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743 AGGGGTGGACGATGCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGT 802
                                                                                              803 CATCGAGAACCATGGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATT 862
                                                                                                                                                                                               863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
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Theses I to 175826.

Murny, D.M., Adams, C., Adio-Oddola, B., Ali-ceman, F. X., Allen, C., Alabrocks, S.L., Aman, C., Are, J.R., Barks, T., Barbaria, J., Blabrocks, S.L., Aman, C., Earnin, D., Bouck, J., Blabrocks, S.L., Aman, E., Bryant, N.P., Buhay, C., Burket, C., Burrell, K.L., Syrd, N.C., Carron, T.E., Erwan, M. Bryant, N.P., Buhay, C., Carron, T.E., Chowdhry, I., Christo, D., Chen, C., Chor, Z., Chowdhry, I., Christo, D., Chen, C., Charl, T.E., David, N.C., Carron, T.E., David, N.C., Carron, T.E., David, N.C., Carron, T.E., Dinh, H.H., Douthwaite, K.J., Dedgado, O., Denn, Z., Chowdhry, I., Dinh, H.H., Douthwaite, K.J., Drapar, H. Dudgan Rochas, S., Durbin, K.J., Barinatt, C., Badgar, D., Edwards, C.C., Blanj, C., Earninatt, C., Edgar, D., Edwards, C.C., Elanj, C., Eascotto, M., Falls, T., Ferraguico, D., Flaggi, D., Borda, J., Garrer, T., Enrandez, J., Harria, P., Harrandez, J., Harria, C., Harrandez, J., Harria, C., Harria, K., Hart, M., Havlak, S., Hame, J., Joackson, E., Jackson, E., Jake, J., Huly, S., Hume, J., Joackson, L.E., Jacobson, B., Jak, Y., Obnson, R., Jollowa, Y., Wallsham, J., Li, J., Li, J., Lide, L., Lieu, C., Lieu, C., Lieu, C., Lieu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, 
                                                                                                                                                                                                                                                                                65820 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 65879
65640 CAGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 65699
                                                                                                                                              65700 AGACCTCATITICTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 65759
                                                                                                                                                                                                                               1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC021890 175826 bp DNA linear HTG 10-NOV-2000 Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,
                                                                                 1043 AGACCTCATTTTCTCCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
                                                                                                                                                                                                                                                                                                                                                                                  1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65880 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 65927
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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KEYWORDS
SOURCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doos/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence it currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13, 108821
Sequencing vector: M13, 108821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 144734 bases at least Q40
Consensus quality: 169424 bases at least Q20
Estimated insert size: 170770, sum-of-contigs estimation
Quality coverage: 0.3 x in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
Acries, X.C.

Direct Submission

Direct Submission

Submitted (22-JAN-2000) Human Genome Sequencing Center, Department Submitted (12-JAN-2000) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2000 this sequence version replaced gi:9719697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21031: contig of 21031 bp in length 21131: gap of unknown length 40475: contig of 19344 bp in length 40575: gap of unknown length 57617: contig of 17042 bp in length 57717: gap of unknown length 75708: contig of 17991 bp in length 75808: gap of unknown length 89018: contig of 13210 bp in length 89118: gap of unknown length 100448: contig of 11230 bp in length 100448: gap of unknown length 100448: gap of unknown length
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unknown length
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of 9211 bp in length
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                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: HMZB
Center clone name: RP11-498A2
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Human DNA sequence from clone RP11-307C12 on chromosome 1, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (09-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                 743 AGGGGTGGACGATGCTGAGATGTGTGCCCTGGACCACTTCGGGGACTTTGACTGGGGT
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             11 172882: contig of 1202 bp in length 172982: gap of unknown length 13 17431: contig of 1449 bp in length 175826: contig of 1295 bp in length 175826: contig of 1295 bp in length. Location/Qualifiers
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171680: gap of unknown length
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.ive 0; Mismatches
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/db_xref="taxon:9606"
/chromosome="3"
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 8, 2002 this sequence version replaced gi:19011396.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORWDEP; Information on the WORWDEP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chr1
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hote="Sequence from overlapping clones RP11-196D4
/A1390204) and RP11-163D16 (AC034149). Assembly confirmed
by restriction digest."
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863 TATCCGCTCCAGACTTTAGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGAGGTGGG 922
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               6955: contig of 4147 bp in length 1455: gap of unknown length 1455: gap of unknown length 1455: gap of unknown length 1455: gap of unknown length 23502: gap of unknown length 3767: contig of 849 bp in length 37867: gap of unknown length 5470: contig of 14265 bp in length 5470: contig of 16603 bp in length 8202: gap of unknown length 8202: gap of unknown length 118932: contig of 27532 bp in length 118932: contig of 27532 bp in length 191318: contig of 27286 bp in length 191218: gap of unknown length 191218: contig of 12186 bp in length 19238: gap of unknown length 19329: contig of 1279 bp in length 192395: gap of unknown length 192395: gap of unknown length
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100.0%; Pred. No. 3.8e-120;
tive 0; Mismatches 0; Indels
unknown length
of 4147 bp in length
unknown length
of 7398 bp in length
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|note="assembly_name:Contig8"
192896. 155189-
|note="assembly_name:Contig9"
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note="assembly_name:Contig11"
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/note="assembly_name:Contigl6"
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/note="assembly_name:Contig12"
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/note="assembly_name:Contig14"
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118933. .191118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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53345 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 53286
                                                                                                      33405 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 53346
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Homo sapiens chromosome 1 clone RP11-163D16, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
                                                                                                                                                1103 AAGGAGGGTGTCTTGGCTTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
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On Sep 1, 2000 this sequence version replaced gi:7579855.
                                                                                                                                                                                                                              1163 CCTCAGCCTGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
                                                               1043 AGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                     53225 GAACCCAGAGCTCCCCAGTGTGGGATACTAATAAACCTCTTGGAGGACA 53178
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Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                         607 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCT 666
                                                                                                                                                                                                                                                                            361 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGARGCCT 420
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                487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 546
                                                                 241 recresacaceaceacereracaaceacererreceaaceacareareceereceereseace 300
                                                                                                                     547 AGAAACGCCAGGCTGACCCCAGGCTTCTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 606
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1 (Dases I to 465)

Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein
Patent: JP 2001269182-A 2126 02-0CT-2001;
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                                                                                                                                                                                                                                                                                                                             667 ATGGGGCCGTGACGCACGGTCCGCGTTGTAGCGTTGGAGCAGA 711
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BD025880
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
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Location/Qualifiers
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JP 2001269182-A/2126
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JP 2001269182-A/2126.
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134171 GGTGGGGCTGACTCTGCAAATGGGGGTGTCCCCCGGATCCTGGCCGAGGTGAGGAACAGA 134112
                                                                                                                                                                                    134051 AGACCTCATTTTCTCCCATGGGGAAGACAGCCATGCTCTTCAGGAGAGACACTCCAAGGGCA 133992
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                                                                                                                                                                                                                                                                                                                                                                                                         13931 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 133872
                                                                                             134111 CAGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 134052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="Maplggaprlyllfsxkrksgkdfytzalgsrlgadycavlrls
gplkegyaqehglnfqrlldtstykbaprkdmirwgebkrqaxxgffcrkivegisqp
iwlysdtrrysdiqwpreaygavtqtvrvaler"
                                              983 CAGGGGGGGTCTAGATTCTGAGGGGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGG 1042
                                                                                                                                                   1043 AGACCTCATTTTCTCCCATGGGGAAGACAGCCATGCTCTTCAGGAGGAGACTCCAAGGGCA 1102
                                                                                                                                                                                                                                                   1103 AAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCC 1162
                                                                                                                                                                                                                                                                                                                                                           1163 CCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAA 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 GATTTTAGGGGTAGGAAAAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGCTCTCTGGTCCACTCAAGGAACACTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 CCCCGCTGGGAGGCGCCCCGCGGCTGGTACTGCTGTTCAGCGGCAAGAGAAAATCCGGGA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 coccecregeagececccecececresiacrecretricaecercaagadaaarcceega 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 AGGACTTCGTGACCCGAGGCGCTGCAGACCAGACTTGGAGCTGATGTCTGTGCTGTCCTCC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATTTTAGGGGTAGGGAGAGTGTCAGCTTCAGGCATCGCGAGGCGTGGCGGCCCCATGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1223 GAACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACA 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 2133 06-SEP-2000;
Genset (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.8%; Score 459.2; DB 6; 98.5%; Pred. No. 5.1e-103; tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AABB6270
Sequence 2133 from Patent EP1033401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/protein_id="CAF00408.1"
/db_xref="GI:40043264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX886270.1 GI:40043263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 98.5%
nes 458; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . >464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX886270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
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VERSION

SOURCE

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us-10-084-817-1.rge

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/note="P-mevalo kinase; Region: Phosphomevalonate kinase. Phosphomevalonate kinase (EC:2.7.4.2) catalyzes the phosphorylation of 2-phosphomevalonate into proposphomevalonate into biosynthesis via the mevalonate pathway. This family represents the animal type of the enzyme. The other is the EGB type, found in plants and fungi, and some bacteria (see pfam00288)"
                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 66 Row: h Column: 3.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 GCTCAGGAGCAIGGCITGAACTICCAGAGACTCCTGGACACCAGCACCIACAAGGAGGCC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 TITCGGAAGGACATGATCCGCTGGGGAGAGAGAAACGCCAGGCTGACCCCAGGCTTCTIT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 İGCCGGAAGATIGIGGAAGGCGIGICCCAGCCIAICIGGCIGGIGAGIGACACACGGAGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756 GCTGAGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCAT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 GCAAAGGAGCATGGCTTGGACTTCCAGAGACTTCTGGATGCGAGCACCTACAAGGAGACC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 GTGTCTGACCATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTT 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 GTAGCGTTGGAGCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGAT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 gergakgreakgregregregakeakerrreggaakerrregaerreggrearreakkeeke 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 816 GGAGTTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.1%; Score 359.6; DB 10; Length 1008; ilarity 72.4%; Pred. No. 2.7e-78; Conservative 0; Mismatches 194; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 1008;
                                                                                                                                                                                                                                                                              tissue type="Mammary gland, lactating clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                            clone="MGC:41584 IMAGE:1247653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="1110011E12Rik protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="synonym: 2900002L22Rik"
db_xref="LocusID:68603"
                                                                                                                                                                                                                                                                                                                                                                    'note="Vector: pT7T3-Pac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="CDD:pfam04275"
                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                              gene="1110011E12Rik"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="MGI:1915853
                                                                                                                                                                                                                                                                                                                                        lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDQLEHLLGFIQAKL"
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                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (basea 1 to 1008)
S trausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Ketteman, M., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1008 bp mRNA linear ROD 06-OCT-2003
IMAGE:1247653), complete cds.
                                                                                                                                                                                                             301 AGAAACGCCAGGCTGNNNCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 360
                                                                                                              241 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGG 300
                                                                                                                                                                     547 AGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCCCAGC 606
                                                                                                                                                                                                                                                                                       607 CCATCTGGCTGGTGAGTGACACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGAGGCCT 666
                                                                                                                                                                                                                                                                                                                                              361 CCATCTGGCTGGTGAGTGACACGGAGAGTGTCTGACATCCAGTGGTTTCGGGARGCCT 420
GGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGCTTGAACTTCCAGAGAC 240
                                                          487 TCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGAGAGGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-APR-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anuradha
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Email: cgapbs.remail.nth.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl.)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                      667 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCAGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGTTGGAGCGGA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC028659.1 GI:20306533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1008)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22388257
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
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                                                                                                           /mol_type="genomic_DNA" .
/db_xref="taxon:9606"
/map="730.7 cR from top of Chr1 linkage group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%; Score 317.2; DB 6; Length 419;
85.6%; Pred. No. 9e-68;
tive 0; Mismatches 3; Indels 67;
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1 (bases 1 to 419)

Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.

EST's and encoded human proteins

Patent: US 6639063-A 3203 28-OCT-2003;
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                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                        733 GCCAGAGGTCTGGGCCAGGATGCTCGTGAGTAGTGGGCAAATAAAGAAACCTCTGGTG--- 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 CTTTAGTGATGAGGCTTGAGGGGACGAGCAGAGACTGATGGGCCTGGCGAACAG-TGGTT 672
                                                                                                                                                                                  847 AGGCGCATGAGTTTTGCCTGAGGCAGGAACATTGCCACACCCATGATGAGGGCAGGCTGCAG 906
                                                                                                               936 CTGCAAAATGGGGGTGTCCC--CCGATCCTGGCCGAGGTGAGGAACAGACAGGGGGGGTC 993
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
1El: 617 252 1900
Fax: 617 252 1902
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STS; STS seguence; primer; seguence tagged site.
Homo sapiens (human)
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Primer B: TGTCTTGGCTGTGGTTGAAG
STS size: 150
PCR Profile:
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Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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Primer: each 5 pM
dNTPs: each 4 nM
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TGCTO	AGACTI		SCICAG	CAG	TTTCGC	TTCGC	GCAGO	GCAGG	FIGTCT 1	STGTC	STAGCO	TAGCC		
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TGGCC	GGAAG	GGAAG	TCCGG	1 1 1	GACTO	GACTO	AGGAG	AGGAG	AGCCC.	AGCCC.	CCTAT	CCTAT		
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                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
DA xref="Laxon:9606"
/noFe="Incyte ID No: 427813.14"
Patent: WO 0177389-A 121 18-OCT-2001;
Incyte Genomics, Inc. (US)
             Incyte Genomics, Inc. (US)
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Best Local Similarity 99.94
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1081 G; 1081 G; 1081 G;	TCCAGTGCATCTGCACAGGCAACGGCC
1141 AGCTGTT	TGCAGACCACGATCGGGATCTGGCCCCTTCACCGATGTTGGT
1141 AGCTGTT	TACCAACCGCAGCCTCACCCCCAGCCTCCTCTA
1201 CAGTGGT 1201 CAGTGGT	STGGTCTACTCTGTG
1261 GCTTTG 1261 GCTTTG	CACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCCAGACTTA 1320
1321 CGGTGG 1321 CGGTGG	CTACAATGGCAGGACGTT 13
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1561	162
1621 C	89.
1681 A	, ,
41 41 1	TGAGGTGCACGTGTGTGGGAATGGTCGTGGGAATGGATGG
1801 0	SCTTCGAGATCAGTGCATTGATGACATCACTTACAATGTGAACGACACATT 1860
1861 0	acarcardaagagacacardcrgaacrgracargcrrcggrcagagg 1920
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Db 3061 GAGTGCAGTGACCGGTGTGAGTGATCCCCGTCAACCTCCTGGCGGCACGG	Qy 3301 TACTGTCCTGGTGAGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT Db 3301 TACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATACCGACTGACCGT Qy 3361 GGGCCTTACCCGAAGAGGCCCAGGCCCAGATACTGTGGGTCCCTCTGTCTCCCAAGTA Db 3361 GGGCCTTACCCGAAGAGGCCCAGGCCCAGGCCAGTACAATGTGGGTCCCTCTGTCTCCCAAGTA	Oy 3421 CCCACTGAGGAATCTGCAGCTGCATCCAGTACACCGTATCCCTCGTGGCCATAAAGGG Db 3421 CCCCCTGAGGAATCTGCAGCTGCATCTGAGTACACGTATCCTTGTGGCCATAAAGGG Oy 3481 CAACCAAGAGGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGGGCTCTAT Db 3481 CAACCAAGAGGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT Db 3481 CAACCAAGAGACCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCCTGGGAGCTCTAT	Qy 3541 TCCACCTTACAACACGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC Db 3541 TCCACCTTACAACACGGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCC Qy 3601 AAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGAGAGAGA	Qy 3661 GACTTCAGGAAGCATCGTTGTGTCCGGGTTGACTCCAGGAGTAGAATACGTCTA Db 3661 GACTTCAGAACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGTAGAATACGTTGTT Qy 3721 CACCATCCAAGTCCTGAGAGATGGACAGGAAAGAAAGAAA	3781 3781 3841	3841 3901 1901	Oy 3991 CIGCACTITICATION	A 981 TGACTGGGATTCACCAACATGGTCCAGACGTGCGTCACCTGGGGTCCACCCCC
	21 AGGCCGTTGGAAGCTACCATGCAGGCCACTTAAACTCCTACACCTAAAAATTCTGT 21 AGGCCGTTGGAAGCTACCATACCAGGCCACCTTAAACTCCTACACCATCAAAGGCCT 21 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACCTTAAACTCCTACACCATCAAAGGCCT 21 AGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCCT 81 GAAGCCTGGTGGTATACGAGGCCAGCTCATCAGCATCCAGCAGAGAGACCTACAAAGAGCCTACAAAGAAACTAAAACTCCTACAGCAGAAAAACTAAAAAAAA	AGTGACTGGTGGTGGTGGTGGTGGGGTCCATCAGCATCCAGCAGTGCGGCCACCAGGA AGTGACTCGCTTTGACTTCACCACCACCAGCACCAGCACCAGGACCACCGT AGTGACTCGCTTTGACTTCACCACCAGCACCAGCACCAGCACCAGGAACACCGT AGTGACTCGCTTTTGACTTTCCCTCTTGTGGCCACCTGTGACCAGCAACACCGT GACAGGAGAGACGACTCCCTTTTTTCTCCTTCTTGTGGCCACTTCTGAATCTGTGACCGAAAT	461 CACAGCCAGTAGCTTTGTGCTCTTTGTGGCCACTTCTGAATCTGGAATCTGGAATCGGAATTCCG	2521 GGTGGAATATGAGCTGAGTGAGGAGGGAGATGAGCCAGTACCTGGATCTTCCAAGCAC 2580 2581 AGCCACTTCTGTGAACATCCCTGACCTGCTCCTGGCCGAAAATACATTGTAAATGTCTA 2640 2581 AGCCACTTCTGTGAACATCCCTGGCTGCTTCGGCGGAAAATACATTGTAAATGTCTA 2640 2641 TCAGATATCTGAGGAGAGAGAGAGTTTGATCCTGTTCAAAAAAAA	2641 TCAGATATCTGAGGATGGGGAGCAGGTTTGATCCTGTCTACTTCACAAACAA	2761 GAGCAGACCCCAGGCTGCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAAGG 2820 2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCGTCACCCTCAGTGACTTGCA 2880 2821 TAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880 2821 TAGCAGCAGAAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCTCAGTGACTTGCA 2880	2881 ACCTGGTGTTCAGTATAACATCACTATGTGTGGAAGAAAATCAAGAAAAGC 2940 2881 ACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAAATCAAGAAAATCAAGAAACC 2940 2941 TGTTGTCATTCAACAAGAAACCACTGGCACCCCAGCTCAGATACAAGAAAACAACAAGAAAATAAAAAAAA	GGACCTGCAGTTTGTGGAAGTGACAGCGTAAGGTCACCATCATGTGGACACGCCTGA

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PD: Ressourcenzentrum, Heubnerweg 6, 14059
, GERMANY; Email: clone@rzpd.de Further
clone and the sequencing project is available
/proj/cDNA/.
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PASBYTVSLVAIKGNOESPKATGVFTTLQPGSSIPPYNTEVTETTIVITWFPAPRIGF
KLGWRBSQGGARAREVTSDSGSIVVSGLTPGYRBYYTTQVLRDGQBRDAPIVNVTT
LSPFTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQGNSLBEVVHADQS
CTFDNLSPGLBYNVSVTVKDDKESVPISDTIIPANPPPDLARTNIGPDTMRYTWAP
PPSIDLTNFLVRYSPVKNEEDVAELSISPSDNAVVLINLLPGTEYVVSVSSVYEQHES
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NGPGFYKTKTAGPDQTEMTIEGLQPYVEYVASYAQNPSGESQPLVQTAVTNIDRPKG
LAFTDVDVDSIKIAMESPGQQVSRYRYVTYSSPEDGIHELFPAPDGEEDTAELQGLRPG
SEYTVSVVALHDDMSSQPLIGTQSTAIPAPADLKFTQYTPTSLSAQMTPPNVQLITYR
VRVTPKEKTIGPMKEINLAPDSSSVVVSGLMVATKYEVSVYALKDTLISRPAQGVVTTL
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PSVGQWIFEBEHGFRATPPPTATPIRHFRPFYPPNVQQEALGGTTIGNAPFQDTSEY
ISCHPVGTDBEPLQFRVPGTTSATLTGLTRGATVII IVBALKDQQHKVRBEVVTV
GNSVREGLNQPTDDSCFDPYTVSHYAVQDEWERNSESGFKLLCQCLGFGSGHFRCDSS
                                                     /translation="GPRRLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPPPT.
LUPPPSWRPQPPGGIRRDPSRRLARBANIVATCHPRAALPHRAMMIRGPGFGGLDLLA
VLCLGTAVPSTGASKRKRQAGWVQPQPSPVAVSQKPPGCYDNGKHYQINQGRETYLL
NALVCTCYGGSRGFNCESKPEDAETCPDKYTGNTYRVGDTYRRPKDSMIWDCTCIGAG
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EENQESTPVVIQQETTGTPRSDTVPSPRDLQPVEVTDVKVTIMMTPPESAVTGYRVDV
IPVNLPGEHGQRLPISRNTFAEVTGLSPGVTYYFKVPAVSHGRESKPLTAQQTTKLDA
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VPHSRNSITLINLIPGTEXVVSIVALNGREESPLLIGQOSTVSDVPRDLEVVAATPTS
LLISWDAPAVTVRXYRITYGETGGNSPVQEFTVPGSKSTATISGLKFGVDYTITVYAV
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QWQXEYLGAICSCTCFGGQRGWRCDNCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTN
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WSKKDNRGNLLQCICTGNGRGEWKCERHTSVQTTSSGSGPFTDARAAVYQPQPPP
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LPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQKYSFCTDHTVLVQTRGGNSNGAL
CHFPPLYNNHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVM
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EEGHMLNCTCFGQGRGRWKCDFVDQCQDSETGTFYQIGDSWEKYVHGVRYQCYCYGRG
IGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSV
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TVTGETTPFSPLVATSESVTEI TASSFVVSWVSASDTVSGFRVEYELSEEGDEPQYLD
LPSTATSVNI PDLLPGRKYI VNVYQI SEDGEQSLI LLSTSGTTAPDAPPDPTVDQVDDT
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ARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIYVIALKNNQKSEPL
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                                                   301 CTGGCCGTCCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGCAAGAGG 360
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3541 CCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATGGACGCCTGCTCCA 3600 3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGAGAGAGA		3722 ACCATCCAAGTCCTGAGAGAGAGAGAGAGAGAGGCGCCAATTGTAAACAAAGTGGTG 3781 	3782 ACACCATTGTCTCCACCAACAACTTGCATCTGGAGGAAACCCTGACACTGGAGTGCTC 3841 		CCTACAAACGGCCAGCAGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC	3962 TGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGTTTACACTGTCAAG 4021 	GATGACAAGGAAAG	GACCTGCGATTCACCAACATTGGTCCAGACCCATGCGTGTCACCTGGGGTCCACCCCCAACATTGGTCCACACATGCGTGTCACCTGGGGTCCACCCCCAAGCGTGTCACCTGGGCTCCACCCAACATGGTCCACACACA	4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201 	4202 GCAGAGITGTCAAITICTCCTICAGACAAIGCAGTGGTCTIAACAAAICTCCTGCCTGGT 4261 	acagaatatgtagt acagaatatgtagt	4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATATTACTGCC 4381 	4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441	4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501	TCCATCACCTCAC CCATCACCCTCAC	4562 AATGGCAGAGAAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621 	4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCACCAGCGTACTGATCAGCTGGGATGCTCCT 4681
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AAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGT 4981 cagredacaccaccaarerreacreacreda 5520 AGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5640 AGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC 5161 GATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5340 AAGCAGACCAGCTCAGGGTGTTGTCACCACTCTG 5700 TCTACAGCTACCATCAGCGGCCTTAAACCTGGA 4801 GGACCAGGACCAACAAAACTAAAACTGCAGGT 5040 GGCTTGCAGCCACAGTGGAGTATGTGGTTAGT 5101 AGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5280 AGIGIGETIGCTICCACGATGATATGGAGAGC 5400 CCAGTGGACACCCCAATGTTCAGCTCACTGGA 5521 SAAGACCGGACCAATGAAAGAAATCAACCTTGCT 5581 AGGACTTATGGTGGCCACCAAATATGAAGTGAGT 5641 CGTGTGACAGATGCTACTGACACCACCATCACC 5761 GTCACTGGCCGTGGAGACAGCCCCGCAAGCAGC GICACTGGCCGTGGAGACAGCCCCGCAAGCAGC 4860 GAAATTGACAACCATCCCAGATGCAAGTGAC 4920 GGACCAGGACCAACAAAACTAAAACTGCAGGT 5041 ACTGATGTGGATGTCGATCAAAATTGCT 5221 ACTGATGTGGATGTCGATTCCATCAAATTGCT 5220 AGGTACAGGGTGACCTACTCGAGCCCTGAGGAT 5281 GATGGTGAAGAAGACACTGCAGAGCTGCAAGGC 5341 AGTGTGGTTGCCTTGCACGATGATATGGAGAGC 5401 GCTATTCCTGCACCAACTGACCTGAAGTTCACT 5461 AAGCAGACCAGCTCAGGGAGTTGTCACCACTCTG 5701 ACTIACGGAGAAACAGGAGGAAAIAGCCCIGIC 4741 GAAATTGACAAACCATCCCAGATGCAAGTGACC 4921

CACATIGCCTGTTCTGCTT 7561 CACATGTCTTGGGAACGGA 7021 TITCTTCTTTCTTABG 7441 FIGURE TO THE TOTAL TO THE PROPERTY TO THE PRO SCATGICTCTCTGCCAAGA 7381 linear PRI 17-JUN-2003 clone DKFZp6860016). TAAGATTTGGTTTGGGAT 7621 AGTGTCTGGCCCGCAATA 7741 AGTGTCTGGCCCGCAATA 7740 CGATGATGGGAAGACATAC 7081 PIGCICCIGCACAIGCITT 7141 regegergaacccaerccc 7201 TACCATCAGAGAACAAC 7261 GTACAGGCTGACAGAGAA 7321 CAGCTTCTCCAAGCATCA 7501 PATCCACAGTACT 7795 ATCCACAGTACT 7794

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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German Genome Project.

This clone (DKFZp6860016) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.

Location/Qualifiers
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LAFTDVDVDSIKIAMESPQGOVSRYRTYSSPEDGTHELPPAPDGEBDTAELQGLRPG
SETVUSVVALHDDMESQPLIGTQSTAI PAPTDLKFTQVTPTSLSAQMTPPNVQLTGYR
VRVTPKEKTGPMKETILADDSSSVVVSGLMVATKYEVSGYALKDTITSRBAQGYVTL
ENVSPPRRARVTDATETITISSMRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYT
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/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWPPPERWRQPPGGIRRDPSRILRREANLVATCLPVRASLPHRIMMLRGPGPGLLLLA
VLCGTAVGPSTGASKSKRQAQQMVQPQSPAVVSQSKPGCYDNGKHYQINQQWERTYLG
NALVCTCTANGSRGFNCBSKPBARETPFKYTGYMYRVGDTYBRPKDGMTWDCTCTGAG
RAISCTIANGGAGSRGFNCBSKPBARETPFKYTGYMYRVGDTYBRFKDSMTWDCTCTGAG
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WSKKDNRGNLLQCICTGNGRGBWKCBRHTSVQTTSSGSGPFTDVRAAVYQPQPPPQPP
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LPFTYNGRIPYSCTTEGRQDGHLWCSTTSNYEQDQKYSFCTDHTVLVQTRGGNSNGAL
RCHPPLYNNGRIPYSCTTEGR&DNHWGSTTQNYEDQKFCPCAPAAHEBICTTTNSGVM
STGDQWDKQHDWGHMAFCCTCVGNGRGEWTCIAYYDADQKFGCPTATTVNVDTFHKRH
BEGHMLNCTCFGQGRCKWCDPVDGCDDSTGTFYQLGDSWBKYVHGYRYQCYCYGG
IGEWHCQPLQTYPSSGGPVEVFITETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSV
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PTPDNLSPBLIEXNVSVYTKODKESVENSDTIIPANPPPILEFTNIGPDIMKVTWAP
PTSPILLFPGLIEXNVSVYTKREEDVAELSISPSDNAVVLTRLLFGTEXVVSYSVSQHES
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LLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKFGVDYTITVYAV
TGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNSISVKWLPSSSPVTGYRVTTTPK
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                            Wiemann, S.
Direct Submission
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landetr.1, D-85764
                                                                                                                                                                Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, I
Mewes, H. W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
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/db_xref="taxon:9606"
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/gene="DKFZp6860016"
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1. .8030
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                                                                                                                 (bases 1 to 8030)
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0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.7%;
Matches 7773; Conservative
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1982 ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2041 1981 ATTGGAGATTCATGGGAAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2040 2042 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGATACCAGTGCTCAGTGGTCT 2101 2041 CGTGGCATTGGGGATTGCCAACCTTTACAGACCTATCCAAGTGGTCT 2101 2041 CGTGGCATTGGGGATTGCCAACCTTTACAGACCTATCCAAGTGGTCT 2100 2102 GTCGAAGTATTTATCACTGAGACTCCGAGTCGAGCCCATCCAGTGGAAT 2161 2101 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACCCCATCCAGTGGAAT 2160 2101 GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACCCCCATCCAGTGGAAT 2160		2342 GTGACTGGGTGTGGGAGGCCAGCTCAGCAGCAGCAGCAGCAGCAGCAACCAGGAA 2342 GTGACTGGCTTTGACTTCACCACCAGCACACCAGCACACCAGCACACCAGCACACCAGTACTGTGACCAGCACACCAGTACTGTGACCAGAAACCAGTACCAGTACTATTCTCCTTTTGTGACCACTTTTTTTT	2461 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTTCGACACTGTGTGGGGATTCGGG 2520 2522 GTGGAATATGAGCTGAGTGAGGGGGAGTTGAGCTATCCAGGATTCCGG 2520 2521 GTGGAATATGAGCTGAGTGAGGGGGAGTTGAGCCACAGTACCTGGATCTTCCAAGCACA 2581 2521 GTGGAATATGAGCTGAGTGAGGGGAATGAGCACAGTACCTGGATCTTCCAAGCACA 2580 2582 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTTAT 2641 2581 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTTAT 2641 2581 GCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTCTAT 2640	CAGATATCTGAGGATGGGAGCAGAGTTTGATCCTGTCTACTTCACAAACAA	
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CATTIGCTCCTGCACATGCTTT 7140 AACGGCCACCCCATAAGGCAT 6481 PAGTGCCACTCTGACAGGCCTC 6661 BAAAGACCAGCAGAGGCATAAG 6720 CAAGCATGTCTCTGCCAAGA 7381 ATGICATCCTGTTGGCACTGAT 6601 Agraccacrergacaggeere 6660 GAAGGCTTGAACCAACCTACG 6781 IGTGAACTACAAGATTGGAGAG 6961 ACCTGGGGGTGAACCCAGTCCC 7201 AGATACCATCAGAGAACAAAC 7260 CAGTGTTGGGCAACAAATGATC 6421 SAAAGACCAGCAGAGGCATAAG 6721 FTACGATGATGGGAAGACATAC 7081 BAGATACCATCAGAGAACAAAC 7261

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please contact the RZED: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzgd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/DNA/.
                                                            7441 CCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA 7500
                                                                                                                                                                                 7501 CCCTGGGAGTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTT 7560
                                                                                                                                                                                                                                                 7562 CGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGAT 7621
                                                                                                                                                                                                                                                                                                                                                                          7681
                                                                                                                                                                                                                                                                                                                                                                                                                                          7621 CAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAA 7680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7681 TritaAgraGGAAAGrCCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATA 7740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSM806171 8035 bp mRNA linear PRI 17-JUN-2003 Home sapiens mENA; cDNA DKFZp686E169 (from clone DKFZp686E169).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemannackfz-heidelberg-de;
sequenced by EWBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                          CAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAA
7442 CCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA
                                                                                                                                                                                                                                                                                                                 7561 CGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITITAAGIAGGAAAGICACCCAAACACTICIGCTITCACTTAAGIGICTGGCCCGCAAIA
                                                                                                                            CCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7741 CIGTAGGAACAAGCAIGAICTIGITACTGIGATATTITAAATATCCACAGTACT 7794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone (DKFZp686E169) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7742 CIGIAGGAACAAGCAIGAICTIGITACTGIGATAITTTAAATAICCACAGTACT 7795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="DKFZp686E169"
note="fibronectin precursor, N-terminus elongated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="CAD97965.1"
/db_xref="G1:31874111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="human cervix"
/clone_lib="686 (synonym: hl
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="DKFZp686E169"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="DKFZp686E169"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 8035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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DHAAGTSYVVGETWEKPYQGWMWYDCTCLGEGSGR.ITCTSRNRCNDQDTRTSYR.IGDT
WASKONRGMLLQCICTGORGSGWKCERHSYQTYSCSGGEFFTDVRAAVYQPQPHPQPP
PYGHYVTDSCYVYSVGWM.KTQGNKQMLCTCLGNGYSCQETAVTOYYGGNSNGEPCV
LPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQXYSFCTDHTVLYQTRGGNSNGAL
CHFPTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQXYSFCTDHTVLYQTRGGNSNGAL
CHFPTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQXYSFCTDHTVLYQTRGGNSNGAL
RTGDQWDXQHDMGHMARCTCVGNGRGBWTCIARYSQLSCOFTHARA
REGRMLNCTCFGGGGGKWKCDPYDQCODSETGTFYYQLGDSWRXYHGYRXYQCYCYGRG
IGEWHCQPLQTYPSSGFVEVPITETPSQPNSHPIQMNAPQPSHISKYILRWRPRNSY
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PASBYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYNTBVTETTIVITWTPAPRIGF
KLGVRPSQGGEAPREVTSDSGNIVVSGLTPGVEYVYTIQVLRDGQERDAPIVNKVVTP
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CTEDNLSPGLEYNVSVYTVKDDKESVPISDTIIPAVPPPTDLRFTNIGPDTWRVTWAP
PPSIDLTNFLVRYSPVKNEEDVAELSISPSDNAVVLTNLLPGTEYVVSVSSVYEQHES
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VPHSRNSITLFNLTPGTEYVVSIVALNGREESPLLIGQQSTVSDVPRDLEVVAATFTS
LLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAV
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NGPGPFKTKTAGPDOTEMTIESLOPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKG
LAFTDVDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTAELQGLRPG
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ARITGYIIKYEKPGSPPREVVPRPRBGVTEATITGLEPGTBYTIYVIALKNNOKSEPL
IGRKKTGSLPOLVTLPHPNLHGPEILDVPSTVQKTPPATHPRYDTGNGIQLPGTSGQQ
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IISCHPVGTDBEPLOFRVPGTSTSATLIGLIRGATYNIIVBALKDQQRHKVRBEVVTV
GNSVNBGLNQPTDDSCFDPYTVSHYAVGDEWBRMSESGFKLLCQCLGFGSGHFRCDSS
                                                                                   LWPPPSWRROPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNWLRCPGFGLLLLA
VLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLG
NALVCTCYGGSRGFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAG
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VRVTPKEKTGPMKEINLAPDSSSVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTL
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OWQXENLGAICSCTCFGGQRGWRCDNCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTN
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translation="GPRRLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPVPFPT/
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1442	TATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACAGTGTTTTGGTTCAGACTCGA 1501
1502	GGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTAC 1561
1562	ACTGATTGCACTTCTGAGGGAGAAGAGACATGAAGTGGTGGTGGTGGGACCACACAGAAC 1621
1622	TATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACA 1681
1682	ACCAATGAAGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGT 1741
1742	CACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTAC 1801
1802	TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
1862	CACAAGOGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
1922	AGGIGGAAGIGIGAICCCGICGACCAAIGCCAGGAITCAGAGACTGGGACGITITIAICAA 1981
1982	ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGAGATACCAGTGCTACTGCTATGGC 2041
2042	CGIGGCAITIGGGGAGIGGCATIGCCAACCITIACAGACCIAITCCAAGCTCAAGGTCCT 2101
2102	GTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCCCCCTCCAGTGGAAT 2161
2162	GCACCAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2221
2222	GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
2282	AAGCCTGGTGTGGTATACGAGGGCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA 2341
2342	GTGACTCGCTTTGACTTCACCACCACCAGCACACACACAC
2402	ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATC 2461
2462	acagccagtagctttgtggtgtgctgggtgtggggttcgacgtgcgggattcgg 2521

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4141 TCCATTGATTTAACCAACTTCCTGGTGGGTTACTCACCTGTGAAAATGAGGAAGATGT 4200 4201 GCAGAGTIGICAATITCICCTICAGACAAIGCAGIGGICTIAACAAAICICCIGGCT 4260 4381 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4440 4501 TCCATCACCCTCACCCCACTCCAGGCACAGAGTATGTGGGTCAGCATCGTTGCTTT 4560 4561 AATGGCAGAGAGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4620 4621 AGGGACCTGGAAGTTGTTGCTGCGACCCCACCCAGCCTACTGATCAGCTGGGATGCTCCT 4680 3841 ACAGTCTCCTGGGAGAGGAGCACCACCACCACCATTACTGGTTATAGAATTACCACAACC 3900 3901 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3960 4081 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4140 4262 ACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4321 4261 ACAGAATATGTAGTGTGTCTCCAGTGTCTACGAACAACATGAGAGCACACCTCTTAGA 4320 4322 GGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTCTGATATTACTGCC 4381 4382 AACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGGATCCGC 4441 4442 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4501 4441 CATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTCGGAAT 4500 4502 TCCATCACCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGCTCTT 4561 4562 AATGGCAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTTCCG 4621 4622 AGGGACCTGGAAGTTGTTGCTGCGACCCCACCAGCCTACTGATCAGCTGGAATGCTCCT 4681 3601 AGAATTGGTTTTAAGCTGGGTGTACGACCAGGGAGGAGGAGGAGAGGCACCACGAGAAGTG 3660 3661 ACTICAGACTCAGGAAACAICGTIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIAGAATACGICTAC 3720 3781 ACACCATTGTCTCCACCAACAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3840 3902 CCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATGCTGATCAGAGCTCC 3961 3961 IGCACTITIGALAACCIGAGICCCGGCCIGGAGIACAAIGICAGIGITIACACIGICAAG 4020 4021 GATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTTCCTCCTCCTCCCACT 4080 4082 GACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGGCTCCACCCCCA 4141 4142 TCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGAGGAAGATGTT 4201 4202 GCAGAGTIGICAATTICTCCTICAGACAATGCAGTGGTCTTAACAAATCTCCTGCCTGGT 4261 3782 ACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGACACTGGAGTGCTC 3841 3842 ACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTATAGAATTACCACAACC 3901 3962 IGCACTITICATAACCIGAGICCCGGCCIGGAGIACAAIGICAGIGIIIAACACIGICAAG 4021 3602 AGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGGAGGCACCACGAGAAGTG 3661 3662 ACTICAGACICAGGAAGCAICGITGIGICCGGCITGACICCAGGAGIAGAATACGICTAC 3721 3722 ACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGTAAACAAAGTGGTG 3781

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5761 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGCC 5820	5822 AATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCACAAGCTACACCATCACT 5881 	5882 GGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGG 5941 	5942 AGCTCCCCTGTGGTCATCGACGCCTCCACTGGTTGATGATGCACCATCCAACCTGCGTTTC 6001	6002 CTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACC 6061	6062 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGTGGTCCCTCGGCCC 6121 6061 GGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCTCGGCCC 6120	6122 CGCCCTGGTGTCACAGAGGCTACTATACTGGCCTGGAACCGGAACCGAATATACAATT 6181 	6182 TATGTCATTGCCCTGAAGAATAATCAGAAGAGAGCGAGCCCCTGATTGGAAGGAA	6242 GACGAGCTTCCCCAACTGGTAACCCTTCCACACCAATCTTCATGGACCAGAGATCTTG 6301	6302 GATGITICCACAGATICAAAAGACCCCTTICGICACCCCTGGGTAUGACACTGGA 6361 	6362 AATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAGCCAGTGTTGGGCAACAAATGATC 6421 	6422 TTTGAGGAACATGGTTTTAGGCGGACCACCGCCCACAAGGGCACCCCCATAAGGCAT 6481	6482 AGGCCAAGACCATACCCGCGAATGTAGGACAAGAAGCTCTCTCT	6542 IGGGCCCCAITCCAGGACACTICTGAGTACAICAITCAIGTCAICCTGTIGGCACTGAI 6601	6602 GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 6661 	6662 ACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCAGCAGGAGGCATAAG 6721	6722 GTTCGGGAAGATGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC	6782 GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAA 6841	6842 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6901
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4682 GCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGTC 4741	. 0 -	CANCARTICACTOR CONTROLLES CANCARACTOR CANCART CASC COCCUTORS CONTROLLES CANCARACTOR CANCAR	AGCCATTTCCATTANTACCAACAAATTGACAAACCATCCAGATGCAAGTGACCACATGACCAGATTGACAAATTGACAAACTTGACAAGTGAAGTGACAAGTGACAAGTGACAAGTGACAAATTGACAAATTGACAAACTCATCCCAGATGCAAGTGACAAATTGACAAAATTGACAAAATTGACAAAATTGACAAATTGACAAATTGACAAATTGACAAATTGACAAATTGACAAATTGACAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAATGACAAATGACAAATTGACAAATTGACAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAATTGACAAATTGACAAATTGACAAAATTGACAAAATTGACAAATTGACAAATTGACAAATTGACAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAAATTGACAAATTGACAAATTGACAAAATTAAAATTAAAATTAAAATTAAAATTAAAATTAAAA	GATGTTCAGGACAACAGCATTAGTGTCAAGTGGTGCTTCAAGTTCCCCTGTTACTGGT 	TACAGAGTAACCACCACTCCCAAAAATGGACCAGGACCAACAAAAACTGAAGGT 	042 CCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGGGGAGTATGTGGTTAGT	GTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCAGACTGCAGTAACCAAC	ATTGATCGCCCTAAAGGACTGGCATTCACTGATGGATGTCGATTCCATTCAAAAATTGCT	TOGGAAAGCCCACAGGCAAGTTTCCAGGTACAGGGAACCTCACCACCACCACAAGTTGCCCACAAAGTTTCCAGGTACAGGTGACCTTACTCGAGGATTACCAAGAAGATTTCCAGGTACAGGTACAGGTACAGTCACCTCAAGCCCCTGAGGATTACCAAAAGTTTCCACAAAGATTACCAAAAAGATTAAAAAAAA	GGAATCCATGAGCTATTCCCTGCACCTGAAGAAGACACTGCAAGCCCTAAGGAAGCAAGC	42 CTCAGACCGGGTTCTGAGTGACAGTGTGGTTGCTTGCACGTGATGATATGGAGGGCTCTTGCACGTTTGTGATATGGAGGGCTCTTGCACGTTGTGATATGGAGGGCTCTTGCACGTTGTGATATGGAGGGCTCTTGCACGTTGTGATATGGAGGGCTCTTGCACGTTTTTTGAGTATATGGAGAGAGTTTTTTGAGTATATATGATATGATATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAGAG	402 CAGCCCCTGATTGGAACCCAGTCCAGGTTTCCTGCACCAACTGACTTCAAGTTCACT	CAGGTCACACCCAAAGCTGAGGGCCCAGTGAACACCCAATGTTCAGGGCTCACTGGAACACCCAATGTTCAGGTCACTGGAACACTGGAACACTGGAACACACCCAGTGAACACACCCAGTGAACACACCCAATGTTTCAGGTCAACACACAC	522 TATCGAGGGGGGGGACCCCCAAGGAGAAGACGGACCAATGAAAGAAA	521 IAICOAGIGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5581 CUIGACAGCICAICCGIGGITGIAICAGGACTIAIGGIGGCCACCAAATAIGAAGIGAGI 5640 5642 GICTAIGCICTIAAGGACACTITGACAAGCAGACCAGCTCAGGGAGTIGICACCACTCTG 5701	702 GAGAATGTCACCCACCACCAAGAAGGGCTCGTGTGACAGACTACCTAC	5701 GAGAATGTCAGCCCACCAAGAAGGGTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760 5762 ATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGCC 5821

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8901 TTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG 6960
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                                                                                                                                                                                                                                                                                                                           7021 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTATGATGATGGAAGACATAC 7080
                                                                                                                                                                                                                                                                                                                                                                                                                                    7081 CACGTAGGAGAACAGTGGCAGAAAGGAAAATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7142 GGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGGTGAACCCAGTCCC 7201
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6841 CGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCAT 6900
                                                                                                                                                                                                                6961 AAGTGGGACCGTCAGGGAGAAATGGCCAGATGATGAGCTGCACATGTCTTGGGAACGGA 7020
                                                                                                                                                                                                                                                                       7022 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGAAGACATAC 7081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6902 ITCAGATGTGATTCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                  7082 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT
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7951 bp mRNA linear PRI 28-AUG-2003
Homo sapiens mRNA; cDNA DKFZp686F219 (from clone DKFZp686F219);
BX640802
                                                                            BX640802.1 GI:34364927
                                                                                                      Homo sapiens (human)
                                                                                                                    Homo sapiens
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 5 HSM806901 ORGANISM

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Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="human cervix"
/clone lib="686 (synonym: hlcc1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHAAGTSYVVGETWEKFYQGWMNDCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDT
WSKKDNRGNLLQCICTGNGRGEWKCERHTSYQTTSSGSGPFTDVRAAVYQPQBEPQPP
PYGHCVTDSGSVYSYGMQMLKTQGNKQMLCTCLGNGYSCQETAVTQTYGGNSNGEPCV
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CHPPPLYNNHNYTDCTSBGRRDNMKNGGTTQNYDADQKSFCTPHTVLVQTRGGNSNGAL
YRIGDQWDKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNNDTFHKRH
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IGBHYQCDPLOTYPSSGGPWYBTITETBPSDNSHIPDWNAPG9BHISKYLTRARFROKSV
GRWKCATIPGHINSYIKGHKPGWYBGQLISIQQYGHGBWTRFDFTTTSTSTFYYSY
TVTGETTPFSPLVATSESVTZITASSFVVSWVSASDTVSGFRVEXELSBEGDEPQYLD
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I PVNLPGEHGQRLPISRNTFAEVTGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDA
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SIVVRWSRPQAPITGYRI VYSPSVEGSSTELNLPETANSVTLSDLQPGVQYNI TI YAV
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7951)
                                                                                                                                                                                                                                                                                                          Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Labbratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                       Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GGCCCGCCCGGCTGTGCTGCACAGGGGAGGAGGAGGAAACCCCAGGCGCGAGCAAG
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project.
This clone (DKFZp686F219) is available at the RZPD in Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="CAE45885.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="fibronectin precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens"
                                                                                                                                                                                                              The German Human cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db xref="taxon:9606"
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Best Local Similarity 98.7%
Matches 7694; Conservative
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JOURNAL
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                                                                         REFERENCE
                                                                                                           AUTHORS
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122 CCCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGCGACACCCCCGGGAGGCATTAGA 181	۵	AGTGGTGTGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGGAAATAAGCAAATG 126
123 CCTTCCCCACCCTCTGGCCCCCACCTTCTTGGAGGGGACAACCCCCGGGAGGCATTAGA 182	Q O ,	AGTGGTGTGGTCTACTCTGTGGGGATGCAGTGGCTGAGGAGACACAAGAAATAAGTG
AGGGATTTTTCCCGCAGGTTGCGAAGGAAGCAAACTTGGTGGCGAACTTGCCTCCCGGTG	λό વ α	1262 CTTTGCACGTGCCTGGCGACGGGGGTCGCTGCTGACGGTGTACCTGTAACCGAACTGTAC 1321 1263 CTTTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCGAGACTAC 1322
183 AGGGATTTTCCCGCAGGTTGCGAAGGAAACTTGGTGGTAGCTAGC	À d	1322 GGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTC 1381
243 cadacáretérecedacereréréakáraráertkádádrecádadecédageregerő 302 302 etgaccaretagaceragagackagagaraceteragagageteregakagagagagagagagagagagagagagagagagagag	& 65 60	TACTCCTGCACCACAGAAGGGCGACAGGACATCTTTGGTGCAGCACCACCTTCGAAT 1
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CAGGCTCAGCAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCA	φ. Q.	1502 GGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCAAC
TGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGGGGGG	γ ο αα	1562 ACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGGACCACACAGAAC 1621
AATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAACCT GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT	yo, du	1622 TATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAATCTGCACA 1681 1623 TATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCAGGAGGAATCTGCACA 1682
GAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAAACACTTACCGAGTGGGTGACACT TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG	Ç. Op	1682 ACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGT 1741 1683 ACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGAAGGGGT 1742
TATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTGGGCGAGGG AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGT	کې	1742 CACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGAATGGACATGCATTGCCTAC 1801
AGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGGTCAGTCCTACAAGTTGGT GACACCTGGAAGAGACCACATGAGACTGGTGGTTACATGTTAGATGTGTGTG	Oy Op	1802 TCGCAGCTTCGAGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTC 1861
GACACCTGGAGGAGCCACCATGAGACTGGTGGTTACATGTTAGAGTGTGTGT	ov du	1862 CACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGC 1921
AATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCT GGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGATGGTA	Qy Db	1922 AGGTGGAAGTGTGATCCCGTCGACCAAGGATTCAGAGACTGGGACGTTTTATCAA 1981
0 0	9.9 2.9	1982 ATTGGAGATTCATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2041 1983 ATTGGAGATTCATGGGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGC 2042
903 GATTGTACTTGCCTGGGAGAGAGCGGGACGCATCACTTGCACTTCTAGAAATAGATGC 962 962 AACGATCAGGACACAAGGACATCCTATAGAATTGGAGAGACACCTGGAGCAAGAATAT 1021	\$ a	2042 CGTGGCATTGGGGGGGTGGCCAATGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2101 2043 CGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCT 2102
963 AAGGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGAATAT 1022 1022 CGAGGAAACCTGCTCCAGTGCATCTGACAAGGGAAACGGCCGAGGAAGAGTGGAAAGTGTGAG 1081	<i>≿</i> 8	2102 GIOGAAGTAITTAICACTGAGACTCCGAGTCAGCCCAACTCCCACCCATCCAGTGGAAT 2161 2103 GIOGAAGTAITTAICACTGAGACTCCCAGCCAACTCCAACTCCCACCCATCCAGTGGAAT 2162
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1083 AGGCACCTCTGTGCAGACCATCAGGGGATCTGGCCCCTTCACCGATGTTCGTGCA 1142 1142 GCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCTCCTGTGTCACAGAC 1201	\$ 6	2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
1143 GTIFITTACCAACCGCAGCCTCAACCCCCAGCTCCTCTATCGCCACTGTGTCACAGAGC 1202	3 & 	AGCCTGGTGTGGTATACGAGGCCCAGCTCATCAGCATCCAGCAGTACGGCCCACCAAGAA

DGGTGCCCACTCTCGGAAT 4501 CCAGCTGTTCCTCCCCACT 4081 ACTITICIGATATTACTGCC 4381 CAGGAGTAGAATACGTCTAC 3721 TCACCTGGGCTCCACCCCA 4141 TGAAAATGAGGAAGATGTT 4201 ATGAGAGCACACCTCTTAGA 4321 ATCACTGGCTACAGGATCCGC 4441 TGCAGCCTGGGAGCTCTATT 3541 CAATTGTAAACAAAGTGGTG 3781 GTTATAGAATTACCACAACC 3901 TCCATGCTGATCAGAGCTCC 3961 TCAGTGTTTACACTGTCAAG 4021 CCCTCGTGGCCATAAAGGGC 3481 GAGAGGCACCACGAGAAGTG 3661 CAATTGTAAACAAAGTGGTG 3781 ACCCTGACACTGGAGTGCTC 3841 GITATAGAATTACCACAACC 3901 CCCTCGTGGCCATAAAGGGC 3481 TCACATGGACGCCTGCTCCA 3601 GAGAGCACCACGAGAAGTG 3661 STCCCTCTGTCTCCAAGTAC 3421

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8 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 8 8 8 8 8
4502 TCCATCACCCTCACCTCACTCCACCCACAGACTATGGTCACACACA	CAGCCCCTGATTGGAACCCCGTCCACAGCTATTCCTGCACCTGACCTGAAGTTCACT 54

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7664 CTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTT	HSM806902 T951 bp mRNA N HCMA DKFZA666K139 (fr	complete dds. BX649182 BX649182.1 GI:34366424		Mammalla; kutheria; frimares; 1 (bases 1 to 7951) Amsorge,W., Krieger,S., Regie: Mewes,H.W., Weil,B., Amid,C.,	The German Human CDNA Consortium Direct Submission Submitted (26-AUG-2003) MIPS, Ingolstaed	Neumelory, Someward Clone from Wiemann, Molecular Genome Research Center (DKFZ); Email s.wiemann@ sequenced by EMBL (European Molecular Bi noidibar/Commann) within the CMM secul	German Genome Project. This clone (DKPZp666K139) is available a please contact the RZBPD: Reseaurcentzentr point in flavilational communications of the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentzentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. Reseaurcentre contact the RZBP. RESEAUrcentr	information about the clone and the sequent at http://mips.gsf.de/proj/cDNA/. Location/Qualifiers		/clone="DKFZp686K139" /tissue type="human cervix" /clone lib="686 (synonym: hlco3	/dev stage="adult" 7951 /gene="DRF2p686K139" 271	/gene="DKYZp686K139" /note="fibronectin precursor" /codon starts	/processin id="CAR46200.1" /bb_xref="G1:34366425" /tb_xref="G1:34366425" /translation="GPRRLCTGGGGGTPGA	UNF FEDRINGE FOR INFO FOR MINISTRANDES POR VICTORY OF A CONTROLL OF A CO	DIFACAL SI VAGET MERE K ÇAMÊMOVOL TOLGE WSKKONKONLLOCI CTORORSGEWKCERHTSK PYGHCVTDSGEVVSVGMOWLKTOGNKOMLCT LPFTYROKETPYSCTTEGRODEHLMCSTTERN CHERTS ANNAHVENTORGEGEB DINAKACCEMP	TERMINIAN SOLD SOLD SOLD SOLD SOLD SOLD SOLD SOLD	GRWAEATI FGHLWST I INCLAFOVY IEGGLI TVTGGTTPRS PLVATSECVTEITAGS FVVSR LPSTATS VNI PDLLPGRKY I VNVY QI SEDGE SIVVRRSPROAPI TGYRI LVYSPSY BGSTEI	EENQEGITVVLQCETIOLEKSDIVESFRUL IPVNLPGEHGQRLPISRNTFAEVTGLSPGV PTNLQLSMKLILLSW"
qq	RESULT 6 HSM806902 LOCUS	ACCESSION VERSION	AEIWOKUS SOURCE ORGANISM	REFERENCE AUTHORS	CONSRIM TITLE JOURNAL	COMMENT		FEATURES			gen							
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6584 ACCAGGGGGCCACCACCAACAACATCATAGTGGAGGCACTGAAAGACCAGCAGGAGGCATAAG 6643.	6722 GTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC	6782 GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGGAA 6841 	6842 CGAATGICIGAAICAGGCITIAAACIGITGIGCCAGGGCTIAGGCTITGGAAGIGGICAI 6901	6902 TTCAGAIGIGATICATCIAGAIGGIGCCAIGACAAIGGIGIGAACIACAAGAITGGAGAG 6961 	6962 AAGIGGGACCGICAGGAGAAAATGGCCAGATGAGCTGCACATGTCTTGGGAACGGA 7021 	7022 AAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGATGGGGAAGACATAC 7081 	7082 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7141 7004 CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 7063	7142 GGAGGCCAGCGGGGCTGGGCGAAACTGCCGCAGACCTGGGGGTGAACCCAGTCC 7201 	7202 GAAGGGACTACTAGGCGAGTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAACAAAC 7261 	7262 ACTANDETTANTECCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGAA 7321	7322 GATTCCGGAGAGTAAATCATCTTTCCAATCCAGGGAACAAGGATGTCTCTGCCAAGA 7381 	7382 ICCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTTCT	7442 CCCTTTGCTCTGGAGGAAGTTCTCCAGGTTCAGCTCAACTCACAGGTTCTCCAAGCATCA 7501 	7502 CCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGGTGCACATTGCCTGTTCTGCTT 7561 	7562 CGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGATTTGGTTTGGGAT 7621 	7622 CAATAGGAAAGCATATGCAGCCAAGATGCAAATGTTTTGAAATGATATGACCAAAA 7681 	7682 TITITAAGTAGGAAAGICACCCAAACACTICTGCTITCACTIAAGTGTCTGGCCCGCAATA 7741 	7742 CTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCACAGTACT 7795
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A linear PRI 30-AUG-2003 from clone DKFZp686K139);
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trum, Heubnerweg 6, 14059
clone@rzpd.de Further
quencing project is available
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                                                                                                                                          ; Vertebrata; Buteleostomi;
ni; Hominidae; Homo.
                                                                                                                                                                           ttmueller, C., Schwager, B.,
A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                    we Analysis, German Cancer m@dkfz-heidelberg.de; Biology Laboratories, quencing consortium of the
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CGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAACTGTGAG GCAGGAAACCTGCTCCAGTGCATCTGCACAGGCCACGGCCGAGGAGAGTGGAAGTGTGAG AGCCACCTCTGCAGCACCACCAGGCCACGGCCCTTCACCGATGTTCGTGCA AGCCACACCTCTGTGCAGCCATCCAGGCCATTCTGCCCCTTCACCGATGTTCGTGCA AGCCACACCTCTGTGCAGCCACCACCAGGCCATCTCACCGATGTTCGTGCA AGCCACACCTCTGTGCAGCCACCACCAGCCCTTCACCGATGTTCGTGCACCTGTTTTCACCAACCCCCACCTGTTCTGCTGCACCTGTTTCACCAACCCCAACCCCCCCC	1382 TACTCCTCACCACAAAAGGCCCACACACACTTCGTCCACCACATTCCAAT 142 1383 TACTCCTCACCACAAAGGCCCACACACTTCGTCACCACACTTCCAAT 142 1442 TATGACCACGACACACACACCTCTTTCTCCACACCTTTTTTGTTTCGACACTTTTTTGTTCCACTTTTTTTT
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3782 ACACCATTGTCT 3782 ACACCATTGTCT 3842 ACACCATTGTCT 3842 ACAGTCTCCTGG 3902 CCTACAAACGGG 3962 TGCACTTTTGAI 3962 TGCACTTTTGAI 3962 TGCACTTTTGAI 4022 GATGACAAGGAA 4082 GACCTGCGATT 4142 TCCATTGATTTI 4142 TCCATTGATTTT 4142 TCCATTGATTTT 4142 TCCATTGATTTT 4161 TCCATTGATTTT 4161 TCCATTGATTTT 4162 GCAGAGTTGTCG 4202 GCAGAGTTGTCGATTGATTTTT 4162 TCCATTGATTTTT 4172 TCCATTGATTTTT 4172 TCCATTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	6 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	2643 CAGATATCTGAGGATACCAGAGTTTGATCCTGTCATTTACAACACAGGGGCC 2702 2702 GATGCCCCTCGAGCCCGACTGAGTTTGATGACCTCTATTGTTGTTGCTGG 2761 2703 GATGCCCCACCTGACCCGACTGAGTTGATGACCTCATTGTTGTTGCTGG 2762 2762 AGCAGCCCCACCTCACGCTCCACAGTTGATGATCATTGTTGTTGTTGCTGG 2762 2763 AGCAGCCCCACCTCACGCTCACAGTTGATAGTTATTGGCATCATTGTTGTTGCTGG 2762 2763 AGCAGCACCACAGCTCCATCACAGTTGATAGTTATTCGCCACCATCAGTAGAAGT 2822 2822 AGCAGCACAGAACTCCATCACAGTACACAACTCATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
3902 CCTACAAACG 	8 8 8 8	AGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCCATCAGTAGAGGTACATCAGTAGGTAG
3782 ACACCATTGT 3842 ACAGTCTCCT (6 6 6	GATGCCCTCCTGACCCGACTGTGGACCAAGTTGATGACCCTCAATTGTTGTTCGCTGG
3722 ACCATCCAAGTC 	& A	GCCACTTCTGTGAACATCCCCTGACCTGCTTCCTGGCCGAAAATACATTGTAAATGTTAA CAGATATCTGAGGATGGGGGGGGGG
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3542 CCACCTTACAAC 3542 CCACCTTACAAC	\$ g	2403 ACAGGAGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATCTGTGACGGAATC 2462 2462 ACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGG 2521 2463 ACAGCCAGTAGCTTTGTGGTCTCTGGGTCTCCAGCTTCCGACACCGTGTCGGGATTCCGG 2522
3482 AACCAAGAGAGC	\dagger \text{43}	
3362 GGCCTTACCCGA 3422 CCACTGAGGAAT	음 강	AAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAA GTGAACTTGGTTATCACCACCACCAGCACCAGCACTGTGACCAGCAGCAGCAGCAGCAGCAGCAGCACGTGACCAACCA
3362 GGCCTTACCCGA	3 8	2223 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAGGCCTG 2282
3302 ACTGTCCTGGTG	& i	2163 GCACCACAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTA 2222 2222 GGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTG 2281
	8 8	2103 GTCGAAGTATTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAAT 2162
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6541 6463	6601 6523	6661 6583	6721	6781	6841	6901	6961	7021	7081	7141	720	c 7261 7183	, 7321	1 7381	7441	7501	T 7561 7483	7621
ATACCCGCCGAATGTAGGACAAGAAGCTCTCTCTCAGACAACCATCTCAAAAAAAA	CATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCTGTTGGCACTCAT 	GAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTCTGACAGGCCTC 	CACCTACAACATCATAGTGGAGGGCACTGAAAGACCAGCAGAGGCATAAC 	GTTCGGGAAGAGGTTGTTACCGTGGCAACTCTGTCAACGAAGGCTTGAACCAACC	GATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAGATGAGTGGGAA 	GAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCCTTAGGCTTTGGAAGTGGTCAT 	(ITCATCTAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAG 	GACCGTCAGGGAGAAAATGGCCAGATGATGATGAGCTGCACATGTCTTGGGAACGGA 	aaaggagaattocaggaaccctcatgaggcaacgtgttacgatgatgatggagaagacatac 	GTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCTGCACATGCTTT 	GGAGGCCAGCGGGGTTGGGGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCCGGTCCC 	aaggcactactggccagtcctacaaccagtattctcagagataccatcagagaacaaa(GTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGGCTGACAGAGA 	GAGAGTAAATCATCTTCCAATCCGGAGGAACAAGCATGTCTCTGCCAAGA 	CATCTAAACTGGAGTGATTAGCAGACCCAGCTTAGAGTTCTTCTTTCT	CTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCTTCTCCAAGCATCA 	CCTGTTCTGCT 	CAATACCGCTCAGTATTTAAATGAAGTGATTCTAAGATTTGGTTTGGGA
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This clone (DKF2661155) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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GSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKGERHTSY
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NYDADQKFGPCPMAAHEBICTTNEGVMYRIGDQWDKQHDMGHMMRCTCVGNGRGEWTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSM806267 8320 bp mRNA linear PRI 17-JUN-2003
Homo sapiens mRNA; cDNA DKFZp686I155 (from clone DKFZp686I155).
BX537590
                                                                                                                                                                                                                    7682 ITITAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGTCTGGCCCGCAATA 7741
                                                                                                                                                                                                                                                               7604 TITITAAGTAGGAAAGTCACCCAAACACTICIGCTITCACTIAAGTGTCTGGCCCGCAATA 7663
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                                                                                         7622 CAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATGACCAAAA 7681
                                                                                                                                                     7544 CAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAATGATATGACCAAAA 7603
                                 7484 cgaagraricaaraccgcrcagrarriraaargaagrgarrcraagarricgarrrgggar 7543
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKP2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstril, D-85764
join(268. 3933,3935. 7609)
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/note="fibronectin precursor, differentially spliced
The frame shift was determined manually"
                                                                                                                                                                                                                                                                                                                                                                                                        7664 CIGIAGGAACAAGCAIGAICITGITACIGIGAIATITITAAATAICCACAGIACI 7717
                                                                                                                                                                                                                                                                                                                                               7742 CIGIAGGAACAAGCAIGAICTIGIIACIGIGAIAITIIAAAIAICCACAGIACI 7795
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/gene="DKFZp686I155"
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join[268. .3933,393
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AUTHORS
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JOURNAL
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II JEVPQLTDLSFVDITDSSIGLRWTPLNSSTIGYRITVVAAGEGT PIEDEVDSSV
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FVEVTDVKVTIKWTPPSSAVTGYRVDVIPVNIPPSPETALFISHUTFPRAQITGYRLT
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Shyjan,A.W.
Methods and compositions for the identification and assessment of
prostate cancer therapies and the diagnosis of prostate cancer
Patent: US 6506607-A 38 14-JAN-2003;
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Sequence 38 from patent US 6506607.
                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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289 TGARACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 334 941 TGARACTGATTCTACTGTGTGAGATGGACTCCACCTCGGGCCCCAGATAACAGGATA 300 349 CCGACTGACTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGCTCCTC 340 349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 340	AGGAATCTGCAGCCTGCATCTC AGGAATCTGCAGCCTGCATCTC AGGAATCTGCAGCCTGCATCTCTC	gagagececaaagecactega 	TACAACACCGAGGTGACTGAG/ 	GGTTTTAAGCTGGGTGTACGA(GACTCAGGAAGCATCGTTGTG1 	CAAGTCCTGAGAGATGGACAG(TTGTCTCCACCAACAAACTTG(TCCTGGGAGAGGAGCACCACC(aacggccagcagggaaattct. 	TTTGATAACCTGAGTCCCGGC(aaggaaagtgtccctatctct 	CGATTCACCAACATTGGTCCAC	GATTTAACCAACTTCCTGGTG(TTGTCAATTTCTCCTTCAGAC/ 	TATGTAGTGAGTGTCTCCAGT(TATGTAGTGAGTGTCTCCAGT	CAGAAAACAGGTCTTGATTCCC
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5929	TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5981
5989	CAACCTGCGTTTCCTGGCCACCACACACATTCCTTGCTGGTATCATGGCAGCCGCCACG 604
6049	TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 610
6109	GGTCCCTGGGCCCGGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 616
6169	CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGAGGGGGCCCCTGATTGG 622
6229	aaggaaaaagacagacgttccccaactggtaaccttccacaccccaatcttcatgg 628
6289	ACCAGAGATCTTGGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCCTGG 634
6349	GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 640
6409	GCAACAATGATCHTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCAC 646
6469	CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAQAAGCTCTCTCTCA 652
6529	GACAACCATCTCATGGGCCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 658
6589	IGITGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 664
6649	TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 670
6709	GCAGAGACCATAAGGTTCGGGAAGATGTTACCGTCGGCACACTCTGTCAACGAAGGCTT 676
6769	GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 682
6829	AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 686

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T680 bp mRNA for fibronectin (FN precursor). X02761 X0055 X00799 X02273 X00307 X00739 X02761.1 GI:31396 alternate splicing; fibronectin. Home sapiens (human)

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [T bases 1 to 788)
Kornblihtt,A.R., Vibe-Pedersen,K. and Baralle,F.E.
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Kornblihtt, A.R., Umezawa, K., Vibe-Pedersen, K. and Baralle, F.E.

Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene
BS284965
2992939
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Human fibronectin: cell specific alternative mRNA splicing
generates polypeptide chains differing in the number of internal
                                                                                                                                                                                                                                                         Kornblihtt, A.R., Vibe-Pedersen, K. and Baralle, F.E. Human fibronectin: molecular cloning evidence for two mRNA specidifering by an internal segment coding for a structural domain EMBO J 3 (1), 221-226 (1984)
                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3218-3222 (1983) 83221567
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	mat_peptide	sc_feature	misc_feature	misc_feature misc_feature	featur	misc_reature	misc_feature misc_feature	misc_feature misc_feature	misc_feature polyA_site	E	Oy 349 GAAGA b . 1 GAAGA	Qy 409 AAGCA Db 61 AAGCA	Oy 469 GACCT Db 121 GACCT	Oy 529 CGAAA Db 181 CGAAA	Qy 589 AGTGG Db 241 AGTGG Qy 649 GGCTC

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ORGANI	AUTHORS 38 TITLE	50 JOURNAL 68 FEATURES 80urce	· · · · · · · · · · · · · · · · · · ·	80 Query Matc Best Local 88 Matches 74	- 61 	48 Db		50 Qy 46	90 E	28	<i>\</i> 6	88 Db 24	40 Oy 64	48 Db 30	00 Qy 70		ð	68 Db 42 20 Qy 82	28 Db 48	80 . Qy 88	88 Db 54	40 QY 94	09 qa	001 KO 100	99 qc	907 106
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Vogel,T., Levanon,A., Werber,M.M.; Guy,R., Panet,A., Hartman,J. and
Shaked,H.
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tive 0; Mismatches 18; Indels 0; Gaps
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4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140 4489 CCACTCTCGGAATTCCATCACCTCACCAACCTCCAGGCACAGAGTATGTGGTCAG 4548 4141 CCACTCTCGGAATTCCATCACCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAG 4200 4549 CATCGTTGCTTCATAATGGCAGAAGAGAAAGTCCCTTATTGATTG	4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728	4441 CCITAAACCIGGAGTIGATTAIACCAICGCGTGGAGACACTGGCGTGGAGACAG 4500 4849 CCCCGCAAGCAAGCCAATTTCCATTAATTACGAACAGAAATTGACAACCATCCCA 4908 4501 CCCCGCAAGCAGCAATTTCCATTAATTACGAACAGAAATTGACAAACCATCCCA 4560 4909 GATGCAAGCAGCAATTTCAGAACAGCATTAATTAGTGCAAATTGACAAATTCCCA 4560 4909 GATGCAAGTGACCGAATTTCAGAACAACAGCATTAGTGCAAGTGCTCCAAATTC 4968 4101	4969 CCCTGTTACTGGTTACAGAGTAACCCCCCCAAAAATGGACCAGGACCAACAAAAC 5028	5089 GTATGTGGTTAGTGTCTAGAATCCAAGGGAGAGAGTCAGCCTCTGGTTCAGAC 5148	5209 CATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGGTGACCTACTC 5268	5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACAGTCAGT	5449 CCTGAAGTTCACTCAGGTCACCCCACAAGCCTCAGGGGCCCAGTGGACACCCCCAATGT 5508
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<i>&</i> 5	5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628 5221 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGACCACAA 5580	8 6	6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAA
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ر م	6409 GCBACBABATGTTTTGAGGBACATGGTTTTAGGCGGACCACACCGCCACBACGGCCAC 6468	y dq	7489 TCTCCAAGCATCACCTGGGGACTTTCCTGAGGC
8 8 8	CCCCATAAGGGATAGGCCAAGACCATACCGCGAATGTAGGACAAGAAGGTCTCTCTC	çy Qı	7549 GCCIGITCIGCITCGAAGIAITCAAIACCGCIC
3 & 5	GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCC 658	λ _O q _O	7609 TTTGGTTTGGGATCAATAGGAAAGCATATGCACATATGCACATATGCACATATGCACAATAGGAAAGCAAAAGGAAAAGCATATGCACAATAGGAAAGGAAAAGCATATGCACAATAGGAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA
3	TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 664	\$ 9	7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACC
đ	6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 6300	ò	7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATG

ATTGACTGCTTCATGCCTTTAGATGTACA 7308 GITCTCCAGCTTCAGCTCAACTCACAGCT 7488 AGCCAACCAAGATGCAAATGTTTTGAAAT 7668 CGCTGTGACAACTGCCGCAGACCTGGGGG 6840 Arctirccaarccagaggaacaagcargr 7020 GGTTTTCTCATAAATGAGGGCTGCACATT 7548 derrircrearaardadddcidcacarr 7200 CCCAAACACTICIGCTTTCACTTAAGIGT 7728 TCTTGTTACTGTGATATTTTAAATATCCA 7788 ACCGTGGGCAACTCTGTCAACGAAGGCTT 6768 TITAAACIGIIGIGCCAGIGCIIAGGCII 6888 AGATGGTGCCATGACAATGGTGTGAACTA 6948 kariegreceareacaaregrereaacra 6600 SAAAATGGCCAGATGATGAGCTGCACATG 7008 GAAAATGGCCAGATGATGAGCTGCACATG 6660 SACCETCATGAGGGAACGTGTTACGATGA 7068 GACCTCATGAGGCAACGTGTTACGATGA 6720 CAGAAGGAATATCTCGGTGCCATTTGCTC 7128 cagaadadarateredargeearrieere 6780 CCCTGTGACAACTGCCGCAGACCTGGGGG 7188 ICCTACAACCAGIATICICAGAGATACCA 7248 ATCTTTCCAATCCAGAGGAACAAGCATGT 7368 ATGITAGCAGACCCAGCTTAGAGTTCTTC 7428 TCAGTATTTTAAATGAAGTGATTCTAAGA 7608 cccaaacacricigcrircacriaagigi 7380 occhacacachtricccarrandccciries 6480 ACATCATAGTGGAGGCACTGAAAGACCA 6708 CCTACACAGTGTCCCATTATGCCGTTGG

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1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068
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      181 CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 240
                                              589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCCATGATCTGGGACTGTACCTGCATCGG 648
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7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440
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28-JUN-1985 B 5 8516421
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CO7K7/10,A61K35/74,A61K37/00,A61K37/04,C07K3/18,C07K13/00, PC
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CI2N15/00,C12P21/00//A61K35/12,(C12P21/00,C12R1:19),(C12P21/00, PC
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                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
1 (Bases 1 to 7705)
Furanshisuko,1.B.
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 7429; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                            linear
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peptide 13 6984
/product='human fibronectin'.
Location/Qualifiers

    .6987
    /product='human fibronectin'

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                                                                                                                                                                                                              RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: JP 1987089699-A 1 24-APR-1987;
DELTA BAIOTEKUNOROJII LTD
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*source: cell_line=Hs 578T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                          E01162 7705 bp cDNA encoding human fibronectin.
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strandedness: Double;
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hypothetical: No;
anti-sense: No;
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JP 1987089699-A/1.
Homo sapiens (human)
Homo sapiens
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1529 GGAAATCTGCACAACCAAT 1321 GGAAATCTGCACAACCAAT 1321 GCATGACATGGGTCACATG 1381 GCATGACATGGGTCACATG 1411 ATGCATTGCCTACTCGCAAG 1441 ATGCATTGCCTACTCGCAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 1501 GAACGACACATTCCACAAG 161	669 GGARATCTGCACAACCAATGAAGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 172 	29 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGAC 1781 	789 AIGCATIGCCIACICGCAGCTICGAGAICAGIGCAFIGTIGAIGACATCACTIACAAIGT 1840 	849 GAACGACACATTCCACAAGCGTCATGAAGAGGGCACATGCTGAACTGTACATGCTTCGG 190 	909 TCAGGGTCGGGGGAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 196	969 GACGITITAICAAAITGGAGAITCAIGGGAGAAGIAIGIGCAIGGIGICAGAIACCAGIG 202 	029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 208	99 CICAAGIGGICCIGICGAAGIAIITAICACIGAGACICCGAGICAGCCAACICCCACC 214	49 CATCCAGTGGAATGCACCAGCCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 220 	209 TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 226	69 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGGAGTA 232 [29 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCAGCACACACA	99 CAGCAACACCGTGACAGGACAGACACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 244	49 IGIGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 250:	509 GTCGGGATTCCGGGTGGAATATGAGCTGAGGAGGAGAGATGAGCCACAGTACCTGGA 256. 	569 TCTTCCAAGCAAGCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCGGCGAAATACAT 262 	29 TGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 268.	689 AACAACAGGGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 274

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49 TGTTGTTGGAGGAGGAGAGCCCCAGGGTCCCATCACGGGTACAGAATAGTCTATTCGCC	01 IGITGTICGCIGGAGGAGACCCCAGGCTCCCATCAGGGTACAGAATAGICTATICGCC 09 AICAGTAGAAGGTAGCAGAGCACAGAACTCAACCTTCAAACTGCAAACTCCGTCACCT	69 CAGTGACTTGCAACCTGGTGTTCAGTATACATCACTATCTAT	29 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 	89 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG	49 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 	09 TGGCGAGCACGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 	69 GICCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGGGAGACCAA 	29 GCCTCTGACTGCTCAACAGACAACCAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 	89 IGAAACIGATICIACIGICCIGGIGAGAIGGACICCACCICGGGCCCAGAIAACAGGAIA 	49 CCAACTGACCGTGGGCCTTACCCGAAGAGGACAGCCGAGGCAGTACAATGTGGGTCCCTC	09 IGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT	69 GGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 	29 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATTGTGATCACATG	89 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGGAGGC 	49 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT	09 AGAATACGTCTACACCATCCAGACTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 	69 AAACAAAGIGGIGACACCAITGICTCCACCAACAAACATGCAICTGGAGGCAAACCCTGA 	829 CACTGGAGTGCTCACAGTCTCCTGGGAGGAGGAGCACCACCCCAGACATTACTGGTTATAG
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3481 CACTGGAGTGCTCACAGTCTCCTGGGAGAGAGCACCACCCCAGACATTACTGGTTATAG 3540	AATTACCACAACCCCTACAAACGGCCAGGGGAAATTCTTTGGAAGAGGGGGCCATGC 3948 	TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008	TIACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068		IGAAAAA IGAAAAA	AACAAA	TGAGAG	ACTITIO DILLII	CACTGG		TGGTCAG	AACAGT	SATCAG	CAGGAGG	AGGAGG	AGACAG	CCCGCGCAAGCAGCAGCAATTTCCATTAATTACCGAACAGAATTGACAACCATCCCA 4908	CCCCGCAAGCAGCCAAGTTTCCATTAATTACCGAACAGAAATTGACAACCATCCA 4550 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968

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ò	7129	CIGCACATGCTTTGGAGGCCAGCCGCGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 7	7188
q	6781		6840
ογ	7189	TGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACCAGCTATTCTCAGAGATACCA 7	7248
qq	6841		6900
δλ	7249	TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7	7308
qq	6901		0969
ζζ	7309	GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7	7368
q ₀	6961		7020
οχ	7369	CICICIGCCAAGAICCAICIAAACIGGAGIGAIGIIAAGCAGACCCAGCIIAGAGIICIIC	7428
Db	7021		7080
λ	7429	TITCTITCTIAGCCCTITGCICIGGAGGAAGIICTCCCAGCIICAGCICAACICACAGCI	7488
Db	7081		7140
λō	7489	TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7	7548
qu	7141		7200
à	7549	GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA	7608
QQ	7201		7260
ò	7609	TITGGITITGGGATCAATAGGAAAGCATATGCGGCGACCAACCAAGATGCAATGTTTTGAAAT	7668
qq	7261		7320
δλ	7669	GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT ;	7728
gg	7321		7380
ò	7729	CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA	7788
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CF455952 15364423 Human Anterior Horn Homo sapiens cDNA clone IMAGE:30515595 5', mRNA sequence. Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo Martination interfaces of nearth, Managarian Gene Correction (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Institute / NIH
Bldg. 31 RmiOA07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at: 1 (bases 1 to 1059) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) CF455952.1 GI:34455608 Homo sapiens (human)

> CF455952 AGENCOURT AL527917 AL527917 AL554310 AL554310 BM808695 AGENCOURT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Lisaue type="Peripheral Nervous system"
/lab_host="DH108 (T1 phage-resistant)"
/lab_host="Human Anterior Horn"
/note="Weetor: pMW-SPORT6.1; Site 1: EcoRV (destroyed);
Site_2: Not1; Library is oligo-dT primed and directionally
closed (EcoRV site is destroyed upon cloning). Average
insert size 2.1 kb. Library was constructed by
Invitrogen."
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http://image.llnl.gov
Plate: NDAM580 row: p column: 04
High quality sequence start: 9
High quality sequence stop: 819.
Location/Qualifiers
1..1059
                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:30515595"
                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="let strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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748 GATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTTCTCCATGGGAAGACAGCCA 807
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1 (bases I to 1150)
1 (Auber, C., Jessee, J. and Polayes, D.
Full.length cDRA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EYRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 530.f For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq=CSODC027AG12QP1kcluster=530.f. Contact :
Feng Librag Email : fliang@lifecen.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CSODC027AG12QP1.
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No. 6.4e-210; 999; Conservative 15; Mismatches 21; Indels 9; Gaps
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CCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCATCCTGACTGGAT 1197
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EST 31-MAY-2003
                 AL554310 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA CLONE CSODIO82YA10 5-PRIME, MRNA sequence.
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RESULT 3
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ACCESSION

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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1. (bases I to 1201)

1. (w.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12894967.
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSOBI082BA0SQP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="amelanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/lone lib="NIH MGC_41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
                        662
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CTGGGGAGAGAAACGCCAGGCTGACCCAGGCTTCTTTGCAGGAAGATTGTGGAGGG 595
                                                                                                                                                                                                                                                                                                                                                                                        843 GGAGCAGTIGGAG-AMCTGATAGAATTTATCCGCTCCAGACTTTAGTCACTAGGTTCTAG 901
                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTGAGCTGGGGCTGCTGGGGGTGGGGCTGACTCTGCAAAATGGGGGTGTCCC 955
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Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nlh.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov

Plate: LLCM1979 row: g column: 01

High quality sequence stori: 15

High quality sequence stori: 695.
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1 (bases 1 to 1080)
1 MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 CCGATCCTGGCCGAGGTGAGGAACAGAGGGGGGGTCTAGATTCTGAGGGGGTTGGT 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 ccariccraccaagaraacamagamagagagarcrararyrgargagargagar 1018
                                                                                                                                          TCGGGAGGCCTATGGGGCCGTGACGCACGGTCCGCGTTGTAGCGTTGGAGCAGAGCCG
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                                                                                                                                                                                                                                                 723 ACAGCAGCGGGGCTGGGTGTTCACGCCAGGGTGGACGATGCTGAGTCAGAATGTGGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db xref="taxon:9606"
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GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                         69.0%; Score 884.4; DB 12; Length 1080; 97.4%; Pred. No. 6.5e-200; ive 0; Mismatches 18; Indels 8;
                                                                                                                                                                                                                                                                                                                  Conservative
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BQ888524 909 bp mRNA linear BST 16-AUG-2002
AGENCOURT_8071320 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090682
5', mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TIGAACTICCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 GAGGGCATCTCCCAGCCCATCTGGCTGATGACACACGGAGAGTGTCTGACATCCAG 650
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                                                               241 CGTGGCGGCCCCATGGCCCCCGCTGGGAGGCCCCCGCGGGCTGGTACTGCTGTTCAGCGGC 300
                                                                                                                                                                               351 AAGAGGAAATCCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 410
                                                                                                                                                                                                                                                                       301 AAGAGGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGAT 360
                                                                                                                                                                                                                                                                                                                                                               411 GTCTGTGCTGCTCCCGCCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCATGGC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGCGC 830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 909)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ888524
BQ888524.1 GI:22280538
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JOURNAL
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/lab host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_112"
/note="Organ: 8%in; Vector: poTB7; Site 1: XhoI; Site 2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
flice BcoRI/XhoI sites using the following 5 adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Superseript II R. (Life Technologies). Note: this is a
NH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT 8050094 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 GCTACGGCGAGGAGGGCGCGATTGTTCCTTGTTGCCGCTCCGCTTAGTGGCCGCGTCCA 230
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                               987 AACCCTCTTGGAGCCTCAAAAAAAAA 1014
                                                                                                 1256 A--CCTCTTGGAGCACAAAAAAAAAA 1281
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/db_xref="taxon:9606"
/clone="IMAGE:6089091"
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AGENCOURT 7047170 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813479
BQ057770
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                                  831 CTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCG-CTCCAGACTTTAGTCACTA-- 887
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 966)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Lou Straut
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.B. Consortium (LINL)
CIONA Library Preparation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
Pitte: LicRos Ill. row: j column: 08
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                  888 GGTTCTAGGAGTGAGCTGGGCCTGCTGAGGTGGGGGTGGGGCTGACT 935
                                                                                                                                                                                                                                                                                                                                                                       841 GGTCTAGGAAGTGAGCTGCGCGCCTTAAAGGGGGGGGTGGGGCCT 888
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/lab_host="DH10B (phage-resistant)
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High quality sequence stop: 705.
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/db_xref="taxon:9606"
/clone="IMAGE:5813479"
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BQ057770
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/lab_host="DH10B (phage-resistant)"
/clone_line="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
inco Eccni/KhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Burkeley) using ZAP-CDNA synthesis Xit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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65.2%; Score 834.8; DB 13; Length 909;
Best Local Similarity 97.7%; Pred. No. 4.2e-188;
Matches 868; Conservative 0; Mismatches 17; Indels 3;
                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
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/db_xref="taxon:9606"
/clone="IMAGE:6089738"
/tissue_type="melanotic melanoma, cell line"
/lab host="DH108 (phage-resistant)"
/clone_lib="NIH MGC_112"
/note="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2:
/note="forgan: skin; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Xit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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http://image.llnl.gov
Plate: LicM3330 row: a column: 03
High quality sequence stop: 698.
Location/Qualifiers
                                                                                                                                                                                                      'organism="Homo sapiens"
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                                                                                                                                                                                                                                    mol_type="mRNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361. CAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
        643 ACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGGGCGGTCCGCGTTGTAGCGT
                                                                                                                                                                                                                                             241 ACATCCAGTGGTTTCGGGAGGCCTATGGGGCCGTGACGCAGACGGTCCGCGTTGTAGCGT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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/lab host="DH10B (phage-resistant)"
/clone="DH10B (phage-resistant)"
/note="Organ: SKin; Vector: pOTB7; Site 1: XhoI; Site 2:
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                                                                                         GCCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACAGGC 780
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1059)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.c. column: 24
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High quality sequence stop: 681.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5516495"
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483 AGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGCTGGGGA 542
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                           543 GAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGCATCTCC
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                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12791409
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477 TICCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTTTCGGAAGGACATGATCCGC 536
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length CDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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BX402738/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 GGGTGTCCCCCGATCCTGGCCGAGGTGAGGNACAGACAGGGGGGGTCTAGATTCTGAGGG 249
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODC027YM23"
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             887 AGGITCIAGGAGIGAGCIGGGGCCIGCIGAGGIGGGGGIGGGGCIGACICIGCAAAAIGG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 AGGTTCTAGGAGTGAGCTGGGNCCTGCTAAGGTGGGGGGTGGGGGCTAACTCTGCAAAATGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 GGTTGGTGGATATTGGGCAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 CGGCAAGAGAAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGAACTTGGAGC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908 CASCGCAAGAGAAATCCGGAAAGAAYTCGTVACCSAGGGGCTGMAGAGCAACTTGGGGC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 TGATGTCTGTGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             848 TGATGTCTGGGCTGTCCTCCGGCTCTCTGGTCCACTCAAGGAACAGTATGCTCAGGAGCA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 IGGCTIGAACTICCAGAGACTCCTGGACACCAGCACCTACAAGGAGGCCTITCGGAAGGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGATCCGCTGGGGAGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGATCCGCTGGGGAGAGGAGAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGAT 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608 CCAGTGGTTTCGGRAGGCCTATGGGGCCATAACGCAGACGGTCCGCGTTGTAGCGTTGGA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707 GCAGAGCCGACAGCAGCGGGGCTGGGTGTTCACGCCAGGGGTGGACGATGCTGAGTCAGA 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAGTTGAACA 826
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Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 530.f For more information about this cluster, see thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSODC027AG12NP1&cluster=530.f. Contact : Feng Liang Email : fliang@lifetech.com URL: this fliang in fliang@lifetech.com INVitroGen.Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODC027AG12NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           827 GCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTTAGTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.6%; Score 827.4; DB 9; Length 1109; ilarity 94.2%; Pred. No. 2.6e-186; Conservative 8; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
xref="taxon:9606"
                                                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 844; Conserv
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1127 GAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCAT 1186
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1067 GACAGCCATGCTCTTCAGGAGAGACTCCAAGGCAAAGGAGGGTGTCTTGGCTGTGCTT 1126
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SX402738 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI082XAIO 3-PRIME, mRNA sequence.
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/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone="colorogyvalo"
/tissue type="ladcenta cor 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Prive prime and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 AAATCCGGGAAGGACTTCGTGACCGAGGCGCTGCAGAGCAGACTTGGAGCTGATGTCTGT 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822 GCTGTCNCCGGNNCTCTNGNNCCACNCAAGGAACAGNATGCNCAGGAGCATGGC-TGAAC 764
                                                                                 188 NACAĞCCATĞCTCTTCAĞĞAĞĞAÇTCCAAĞĞĞCCAAAĞĞAĞĞĞTĞTCTTĞĞCTĞTĞCTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     941 GGCCCWATGKCYCCGYTGGGAGTCTCCCCGCGTCTKGSACTTCTTTTCWGCGGCAAGAGG 882
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                                                                                                                                                                                                                                                                            128 GAAGGCGAAACCCTGCCATATCCCCAGTGCCAGTCCCCTCAGCCTGTGGTGGCCTTGCAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 530.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                   1187 CCTGACTGGATGTTCTCAGCCCCTTGTTCTGGGCAAGAACCCAGAGCTCCCCAGTG 1242
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cgi-bin/cluster.cgi?seq=CSIAI021ZC06NP1&cluster=530.f. Contact
cgi-bin/cluster.cgi?seq=CSIAI021ZC06NP1&cluster=530.f. Contact
Feng Liang Email : fliang@lifetech.com W.R. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI021ZC06NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               68 CCTNACTGGATGTTCTCAGCCCCTTGTTCTGNGCAAAACCCAGNGTCCCAGTGTG 13
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DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                             db_xref="taxon:9606"
/clone="IMAGE:6211288"
                                                                                                                                                                                           /mol_type="mRNA"
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                         Trecagagaerenrigaacaccageaceaseaagaagageerriregaaggacargancege 704
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                                                                    TGGGGAGAGAGAAAACGCCAGGCTGACCCAGGCTTCTTTTGCAGGAAGATTGTGGAGGGC
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Contact: Robert Strausberg, Ph.D.
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/note=_Organ: allyary gland; Vector: poTB7; Site_1: Xho1; Site_2: EccR1; cDNA made by oligo-dT priming.
Directionally cloned into EccR1/Xho1 sites using the following S' adaptor: GGCACGAG(0). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies), Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLCM373 row: i column: 17
High quality sequence stop: 651.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC_102"
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Homo sapiens (human)
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/tab host="DH1036 (phage-resistant)"
/clone_lib="NHH MGC Lib"
/note="Corgan: skin; Vector: pOTB7; Site_l: XhoI; Site_2:
/note="Corgan: skin; Vector: pOTB7; Site_l: chord line Decal; DANA made by o ligo-dr priming. Directionally cloned into EccR1/XhoI sites using the following 5' adaptor:
/GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Barkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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                                  661 AGTCAGAATGTGGCCTGNACAACTTCGGGGACTTTGACTGGGTCATCGAGAACATGGAG 720
                                                                                                                                        880 AGTCACTAGGTTCTAGGAGTGAGCTGGGGCCTGCTGA--GGTGGGGGTGGGGCTGACTCT 937
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2500 row: e column: 10
High quality sequence start: 6
High quality sequence start: 6
High quality sequence stop: 593.
 760 AGTCAGAATGTGGCCTGGACAACTTCGGGGACTTTGACTGGGTCATCGAGAACCATGGAG
                                                                     820 TTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTT
                                                                                                       721 TTGAACAGCGCCTGGAGGAGCAGTTGGAGAACCTGATAGAATTTATCCGCTCCAGACTTT
                                                                                                                                                                            781 AGTCACTAAGTTCTAGTAATGAGCTGGGGCCTCCTGAAGGTGGGGGGTGGGGGTTGACTCT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                841 GCCAAAAGGGGGGGGGCCCCCCATCCTGGCCCCGGTGGAACAAAAAACCGGGGG 895
                                                                                                                                                                                                              63.8%; Score 817.2; DB 13; Length 930; 97.3%; Pred. No. 6.6e-184; ive 0; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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5', mkNA sequence.
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(clone lib="NNH MGC 99"
| note="Organ: lymph vetor: pOTB7; Site 1: XhoI; Site 2: hote="Organ: lymph vetor: poTB7; Site 1: XhoI; Site 2: EcoR1; cDNA made by oligo-dr priming. Directionally cloned into EcoR1/XhoI sites using the following 5; dataptor: gGCACGAG(G). Size-selected >500bp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript IR R. (Life Technologies). Note: this is a NIH_MGC
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                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2083 row: j column: 21
High quality sequence stop: 623.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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95.5%; Pred. No. 8.5e-184;
tive 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5920244"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                               Contact: Robert Strausberg, Ph.D.
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JOURNAL
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Confect: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Neb: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 530.f For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi-bin/cluster.cgi?seq-c5000014DF12QP1&cluster=530.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://hlllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DC014DF12QP1.
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ALS26453 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DC014YL24 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1084 GGAGGAGACTCCAAGGGCAAAGGAGGGTGTCTTGGCTGTGCTTGAAGGCGAAACCCTGCC 1143
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                                                                                                                                                                                                                                                                                                       964 GGCCGAGGTGAGGAACAGACAGGGGGGTCTAGATTCTGAGGGGGTTGGTGGATATTGGG 1023
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Five prime end enriched, double-strand cDNA was digested with not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                          601 GECCEAGETGAGGAACAGACAGGGGGGTCTAGATTCTGAGGGGGGTTGGTGGATATTGGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 caaggcaggaaactronggagactroarringrocargggaagacagccargcrorrca 720
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TOGGGCCTGCTGAGGTGGGGGTGGGGCTGAAATGGGGGTGTCCCCCGATCCT 963
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1 (bases 1 to 1031)

1 (M.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12789946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1024 CAAGGCAGGAAACCTCTGGAGACCTCATTTTCTCCATGGGGAAGACAGCCATGCTCTTCA
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/db_xref="taxon:9606"
/clone="CSODC014YL24"
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1064 GAAGACAGCCATGCTCTTCAGGAGGAGACTCCCAAGGCAAAGGAGGGTGTCTTGGCTGTG 1123
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Query Match 63.7%; Score 816.4; DB 9; Length 1031;
Best Local Similarity 99.9%; Pred. No. 1.1e-183;
Matches 817; Conservative 0; Mismatches 1; Indels 0; Gaps
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TYPE: DNA ORGANISM: Homo sapiens
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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99.9%; Pred. No. 0;
tive 0; Mismatches 9; Indels 0;
                                                                                           APPLICANT: Loring, Jeanne F.
APPLICANT: Loring, Jeanne F.
APPLICANT: Loring, Jebora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/05/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
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OTHER INFORMATION: Incyte ID No. 6682888 427813.14
; Sequence 135, Application US/09566921
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95.2%; Score 7423; DB 4; Length 7679;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7432; Conservative 0; Mismatches 15; Indels 0;
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                     SEQ ID NO 38
LENGTH: 7679
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 07334-074001
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CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
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2520 2928 2988 2640 3168 3001 CCGACTGACCGTGGGCCTTACCCGAAGAGCCAGCCCAGGCAGAACAATGTGGGTCCCTC 3060 2521 cagreactriscaaccrissistricasraraacarcactarcrariscrississaaaarca 2580 2700 2820 2881 GCCTCTGACTGCTCAACAGACAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940 2941 reakakorgantonakorgickindangaandeakorokakorokadanakokadana 3000 3349 CCGACTGACCGTGGGCCTTACCCGAAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408 3409 TGTCTCCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468 2508 2160 2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628 2629 IGTAAATGICTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688 2281 IGHAAHGICTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2340 2689 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2748 2341 AACAACAGGGCCTGATGCCCCTCCTGACCGGACTGTGGACCAAGTTGATGACACTCAAT 2400 2749 IGIIGIICGCIGGAGCAGACCCCAGGCICCCAICACAGGGIACAGAAIAGICIAIICGCC 2808 2401 rerrerresadesadesadesecesadeseresenteseadadadadana retratedes 2460 2809 ATCAGTAGAAGGTAGCAGAGAGCTCCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868 3048 2760 2161 Gredddarrecdddrafardaddraddraddaddaddaraddaddeddadraecheda 2220 2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCACCACCAGCACACCCGTGAC 2388 2389 CAGCAACACCGTGACAGGAGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448 2461 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCC 2641 GCCTCTCCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACGCATCATGTG 3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2581 AGAAAGTACACTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3049 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCCGTCAACCTGCC 2701 gacaccecercadadadeadadeacederaccercadadaroroarcecercaderece 3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2761 rescenses es de constante de constante de la reconstante del la reconstante del la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de la reconstante de 3229 GCCTCTGACTGCTCAACAGACAACCTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2101 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGGTTCCGACACGGT 2221 TCTTCCAAGCACACCACTTCTGTGAACATCCCTGACTGCTTCCTGGCCGGAAAATACAT 2041 cadcaacaccerdacadadadadacrecerrrrerecrerrereredecacrecesare 2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT

1 CCACTCTCGGAATTCCATCACCTCACCACCTCACTCCAGGCACAGAGTATGTGGGTCAG 420	49 CATCCTTGCTCTTAATGGGAGAGAAACTCCCTTATTGATTG	09 TICTGAIGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCCCCC	69 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 	9 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGGAGCAAGTCTACAGCTACCATCAGCGG 478 	CCTIAAACCTGGAGTIGATIAIACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAG 4	4849 CCCGGCAAGCAAGCCAATTTCCATTAATTACGAAAATTGACAAACGTCCCA 4908 	9 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 496 	9 CCCTGTTACTGGTTACAGAGTAACCACCACCACAAAATGGACCAGGACCAACAAAAC 502 	5029 TAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGTGGA 5088	5089 GTATGTGTTAGTGTCTAGAATCCAAGGGGAGAGAGTCAGGCTCTGGTTCAGAC 5148	5149 TGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGATTC 5208	9 CATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGTGACCTACTC 526 	5269 GAGCCCTGAGGATGGAATCCATGAGCTATTCCCTGCACCTGATGGTGAAGAAGACACTGC 5328	5329 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGT	5389 TGATATGGAGACCCGGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA 5448 [CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACTGTTTTTTTT	5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACGGGACCAATGAAAGA 5568	5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628
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949 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 1008
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                                           241 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300
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                                                                                                                    649 GGCTGGGCGAGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 708
                                                                                                                                                                     301 GGCTGGGCGAGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 360
                                                                                                                                                                                                                                                                                   361 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 420
                                                                                                                                                                                                                                                                                                                                        TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAAAGTGTTT 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                829 TGATCATGCTGCTGCTGCGTTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGG 888
           589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG
                                                                                                                                                                                                                            CTACAAGATTGGTGACACCTGGAGGAGCCACATGAGACTGGTGGTTACATGTTAGAGTG
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APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                       E: INCYTE PHARMACEUTICALS, INC. 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA-0001 US
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                                                                                                                                                       Sequence 1289, Application US/09023655
Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1289:
SEQUENCE CHARACTERISTICS:
LENGTH: 7680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                1508
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
7441 CAGTACT 7447
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STATE: CALIFORNIA
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LIBRARY: GENBANK
                                                                                                                                                                                                                      GENERAL INFORMATION:
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IS-09-023-655-1289
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                                                                                                                                     18-09-023-655-1289
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Version #1.30 (EPO)

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SCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840
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                                                                                                                                                                                                                                                                                                                                                          95.2%; Score 7423; DB 5; Length 7680; 99.8%; Pred. No. 0; Live 0; Mismatches 15; Indels 0.
           REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD=1A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 7680 base pairs TYPE: nucleic acid STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Matches 7432; Conservative
                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
CT-US95-09819-6
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Best Local Similarity
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CTACAGGATCGGCCATCATCCGAGGACTTCAGTGGGAGACC CTACAGGATCGGCATCATCCGAGCACTTCAGTGGGAGACC CCACTCTCGAATTCCATCACCCTACCACCACCTCACTGGGGAGACC CCACTCTCGGAATTCCATCACCCTCACCACCTCACTCCAGG CATCGTTGCTCTTAATGGCAGAGAGAAATCCCTTATTGAT CATCGTTGCTCTTAATGGCAGAGAGAAATCCCTTATTGAT TTCTGATGCTCTTAATGGCAGAGAGAATGTTGCTTGTTGTT TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCC TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCC CTGGGATGCTCCGAGGGACCTGGAAGTTGTTGCTGCTGCGACCCC CTGGGATGCTCCTGCTGCACAGGAAGTTGTTGTT TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCC CTGGGATGCTCCTGCTGCACAGTGAATTACAGGACCCC CTGGGATGCTCCTGCTGCACAGTGAATTACAGGACCCC CTGGGATGCTCCTGCTGCACAGTGAATTACAGGATCAC	AAATAGCCTG AAATAGCCTG AAATAGCCTTG CCTTAAACCTG CCTTAAACCTG CCCCGCAAGCA	0 0-0 0-0 1-1	AAAACIGGAGGTCAGATCAAACAGAATGACTATTGAAGG THTGTGGTTAGTGTTATGCTCAGAATCCAAGGGGAGAGAGA TATGTGGTTAGTGTTATGTCTCAGAATCCAAGGGAGAGAGA	

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CGCCACG 6048 CGGGAAC 6168 TGATTGG 6228 |||||||| |TGATTGG 5880 TTCATGG 6288 |||||||| TTCATGG 5940 ACCCTGG 6348 ||||||| ACCCTGG 6000 SCTACTGA 5748 AAGTTGA 5808 ||||||||| |AAGTTGA 5460 GAGAAGT 6108 |||||||| |GAGAAGT 5760 GTCATCC 6588 |||||||| GTCATCC 6240 GTGTTGG 6408 |||||||| GTGTTGG 6060 TCTCTCA 6528 |||||||| TCTCTCA 6180 TGAAAGA 5568 CAGAAG 5868 CTTGAA 5580 TGCCAC 6648 rdaaada 5220 AGGGAGT 5688 CAGAAG 5520 CCTTGAA 5928 |||| || || AGGGTGT 5340 GGCCAC 6468 |||||| |GGCCAC 6120

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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        RESULT 5
US-08-259-569-16
; Sequence 16, Application US/08259569
...tent No. 5679320
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECONTUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vogel, Tikva
APPLICANT: Levanon, Avigdor
APPLICANT: Werber, Moshe
APPLICANT: Guy, Rachel
APPLICANT: Panet, Amos
APPLICANT: Panet, Amos
APPLICANT: Barkman, Jacob
APPLICANT: Shaked, Hadassa
TITLE OF INVENTION: FIBRIN BII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 7705 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-MAY-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                  7789 CAGTACT 7795
                                                                                                                                                                               7441 CAGTACT 7447
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STREET: 30 AL
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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US-08-259-569-16
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6241 TGTTGGCACTGATGAAGAACCCTTACAGTTCCTGGAACTTCTACAGTGCCAC 6300
                                                                    6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 6708
                                                                                                      6301 TCTGACAGGCCTCACCAGGGGGCCACCTACAACATCATAGTGGAGGAGCACTGAAAGACCA 6360
                                                                                                                                                            6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 6768
                                                                                                                                                                                    6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 6828
                                                                                                                                                                                                                                                                                          6421 GAACCAACCIACGGAIGACICGIGCITIGACCCCIACACAGITICCCAITAIGCCGITGG 6480
                                                                                                                                                                                                                                                                                                                                     6829 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6888
                                                                                                                                                                                                                                                                                                                                                                               6481 AGATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTT 6540
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7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440
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7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380
                                                                 7729 CIGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
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95.2%; Score 7418.2; DB 1; Length 7705;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7429; Conservative 0; Mismatches 18; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRIN BINDING DOMAIN POLYPEPTIDES AND USES AND METHODS OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,569
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>	469 GACCTACCTAGGCAATGCGTTGGTTTGTTTTTGTGGAGGAAGCCGAGGTTTTAACTG 528	& <u>8</u>	1549 CAACCACATTACACTGATTGCACTTCTGAGGGCAGAAGAGACA.
, ,	CGAAAGTAAACCTGAAGGGGGGTTGCTTTGACAAGTACACTGGGAACACTTACCC 	දි සි	1609 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCC
, 5 . 0	89 AGTGGGTGACACTTATGAGGGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 41 AGTGGGTGACACTTATGAGTGACTCTAAAGACTCCATGATCTGGAACTGTACCTGCAATCGA	& a	1669 GGAAATCTGCACAACGAAGGGGTCATGTACCGCATTGGAG
)	49 GGCTGGGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAGGGGGTCGGTC	\$ <u>8</u>	1729 GCATGACATGGGTCACATGATGAGGTGCACGTGTGTTGGGAATGC
· > ^	CTACAAGATTGGTGACACCTGGAGGAGCCACATGAGACTGGTGGTTACATGTTAGAGTG	& <u>a</u>	1789 AIGCATIGCCTACTCGCAGCTICGACAICAGIGCATIGTIGAIGAIGAIGAIGAIGAILA AIGCATIGCCTACTCGCAACTICGAGAICAGIGCAIGAIGAIGAIGAIGAIGAIGAIGAIGAIGAIGAIGAIGA
5 . 0	769 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAGTGTTT 828 	දු පු	1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGA
5. 0		& 9	1909 TCAGGGTCGGGGCAGGTGGAAGTGTGATCCCGTCGACCAATGCCJ
5 - 0	CTGGATGATGGTAGATTGTACTTGCCTGGAGAAGGCAGCGGACGCATCACTTGCACTTC CTGGATGATGATAGTTGTACTTGCCTGCGAAAGGCAGCGAACGCATCACTTGCACTTC CTGGATGATGGTAGATTGTACTTGCCTGCGAAAGGCAACGGAACGCATCCACTTGCACTTGCAAAAGCAAGGCAACGAACCATTGCACTTGCACTTGCACTT	λo q	1969 GACGTTTTATCAAATTGGAGATTCATGGGAGAAGTATGTGCATGG
~ ^	949 TAGAAATTAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTTGGAGACACCTGGAG 1008	දු පු	
>- ^	1009 CAAGAARAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCGAGGAGA 1068 	જે <u>વ</u>	2089 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCT
5 . 0	GTGGAAGTGTGAGAGGCACCTCTGTGCAGACCACATCGAGCGAATCTGGCCCTTCAC	& 43	2149 CATCCAGTGGAATGCACCACAGCCATCTCACATTTCCAAGTACA:
>- ^	CGATGTTCGTGCAGCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTATGGCCA 	& 8	9 TAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCA
۵ .<	1189 CTGTGTCACACACAGTGGTGTGGGGTCTACTCTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248 	& g	2269 CATCAAAGGCCTGAAGCCTGGTGGTATACGAGGGCCAGCTCAN
۵ خ	AAATAAGGAAATGCTTTGCACGTGCCTGGGAAGGGAGTCAGCTGCCAAGAGACTGT	O O O	TTCACCACCACC
۵ د ٠	AACCCAGACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA AACCCAGCTTACGGTGGCCAACTTAAATGGAGAGCCATCTGTCTTACCATTCACCTACAA	که و _۵	CAGCAACACCGTGACAGGAGGACGACTCCCTTTTCTCCTCT
۵ ۸	1369 TGGCAGGACGTTCTACTCCTGCACCACAGAAGGCGACAGGACGGAC	S S	2449 TGTGACCGABATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTC 2101 TGTGACCGABATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTC
۵ خ	9 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1	o Q	2509 GTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGAGGGGGAGATG;

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GGTGTCAGATACCAGTG 2028 TTACAGACCTATCCAAG 1740 CAGGATTCAGAGACTGG 1968 TTACAGACCTATCCAAG 2088 CAGCCCAACTCCCACCC 2148 CAGCCCAACTCCCACCC 1800 ACCAGCACACCTGTGAC 2388 GAGCCACAGTACCTGGA 2568 Trecerrectaracaa 1548 CCCATGGCTGCCCACGA 1668 GATCAGTGGGATAAGCA 1728 GGTCGTGGGGAATGGAC 1788 AACTGTACATGCTTCGG 1908 ATTCTCAGGTGGAGACC 2208 CACTTAAACTCCTACAC 2268 CACTTAAACTCCTACAC 1920 Arrerederedadece 1860 ATCAGCATCCAGCAGTA 2328 GIGGCCACTICTGAATC 2448 TCAGCTTCCGACACCGT 2508

4729 AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGGG 4788 3301 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3360 3709 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3768 3361 AGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAATTGT 3420 3769 AAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCCTGA 3828 3421 AAACAAAGTGGTGACACCATTGTCTCCACCAACAACTTGCATCTGGAGGCAAACCTGA 3480 3829 CACTGGAGTGCTCACAGTCTCCTGGGAGAGGACCACCCCCAGACATTACTGGTTATAG 3888 3481 cacigoagracicacagicicciosoagagoagocaccaccocagacatraciogrianas 3540 3889 AATTACCACAACCCCTACAAACGGCCAGCAAGAAATTCTTTGGAAGAAGTGGTCCATGC 3948 3541 AATTACCACAACCCCTACAAACGGCCAGCAGGAAATTCTTTGGAAGAAGTGGTCCATGC 3600 3949 IGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4008 4009 TIACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGT 4068 3661 Tracacrercaaggargacaaggaaagrerccrarcrercaraccarcarccaecrer 3720 TCCTCCTCCTCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128 3721 TCCTCCCACTGACCTGCGATTCACCACATTGGTCCAGACACCATGCGTCACCTG 3780 4129 GGCTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 4188 3781 GGCTCCACCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAA 3840 4189 TGAGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAA 4248 3841 readgaagargrigcagagrigrcaarrrcrccrrcagacaargcagrggrcrraacaaa 3900 4249 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAG 4308 3901 TCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCCAGTGTCTACGAACAACAACAAGAG 3960 4309 CACACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTT 4368 3961 CACACCICITAGAGGAAGACAGAAAACAGGICITGATICCCCAACTGGCAITGACTITIC 4020 4369 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4428 4021 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGG 4080 4429 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4488 4081 CTACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCC 4140 4489 CCACTCTCGGAATTCCATCACCCTCACCAACCTCCAGGCACAGAGTATGTGGTCAG 4548 4141 CCACTCTCGGAATTCCATCACCTCACCAACCTCAAGGCACAGGCATATGTGGTCAG 4200 4201 CATCGTIGCTCTIAATGGCAGAGAGGAAGTCCCTIATIGATTGGCCAACAATCAACAAGT 4260 4261 TrongandiroccadededeconddaadrichiecnecadoccodoccadocracteardaG 4320 4669 CTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGG 4728 3601 TGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT 4069 셤 셤 d a q ઠે 엄 유 g ò 셤 ઠે d ò a ઠે g ઠે ઠે 원 ઠ 셤 ઠે 셤 ઠ ò ઠે 엄 ઠે ò ద ò ઠે 2221 TCTTCCAAGCACACCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2280 2689 AACAACAGGGCCTGATGCCCCTCTGACCGGACTGTGGACCAAGTTGATGACACCTCAAT 2748 2641 GCCTCTCCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 2700 3049 GACACCCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGATCCCCGTCAACCTGCC 3108 2821 GTCCCCTGGGGTCACTATTACTTCAAAGTCTTTGCAGTGAGCCATGGGAGGAGAGCAA 2880 3229 GCCTCTGACTGCTCAACAGACAACAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 3288 2881 GCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCTCCAGTTTGTCAA 2940 3289 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3348 2941 TGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAGATAACAGGATA 3000 3001 CCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATGTGGGTCCCTC 3060 3409 IGTOTOCAAGTACCCACTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3468 3529 IGGGAGCICIAITCCACCITACAACACCGAGGIGACTGAGACCACCAITGTGATCACATG 3588 3181 TGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGATCACATG 3240 3589 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGGAGGAGGAGG 3648 3241 GACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGGGTGTACGACCAAGCCAGGGAGGAGGAGGAGGA 3300 3649 ACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCAGGAGT 3708 2569 TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628 2629 IGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGAGTTTGATCCTGTCTACTTCACA 2688 2281 TGTAAATGTCTATCAGATATCTGAGGATGGGGGAGCAGCAGTTTGATCCTGTCTACTTCACA 2340 2341 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT 2400 2749 IGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808 2401 TGTTGTTGGCTGGAGCAGGCCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2460 2809 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCT 2868 2521 CAGTGACTIGCAACCTGGTGTTCAGTATAACATCACTATCTATGCTGTGGAAGAAATCA 2580 2581 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT 2640 2989 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048 2701 GACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGGATGTGATCCCCGTCAACCTGCC 2760 2761 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2820 3349 CCGACTGACCGTGGGCCTTACCCGAAGAGGACAGCCCAGGCAGTACAATGTGGGTCCCTC 3408 3061 TGTCTTCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGTATCCCTCGT 3120 3469 GGCCATAAAGGGCAACCAAGAGAGCCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3528 3121 GGCCATAAAGGGCAACCAAGAGGCCCCCAAAGCCACTGGAGTCTTTACCACACTGCAGCC 3180 2461 ATCAGTAGAAGGTAGCAGCACAGAACTCCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 3109 TGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCAGAAGTCACCGGGCT 2929 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCACGCTCAGATACAGT

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≵ 4	4789 CCTTAAACCTGGAGTTGATTATACCATCACTGGTGTGTGT	q ₀	
≯ ₩	4849 CCCGGCAAGCAAGGCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCA 4908	충 옵 ·	5581 TGACAATGCTCGGAGCTCCCTGTGGTCATCGACGCTCTGTGTTTTTTTT
≵	4909 GAIGCAAGTGACCGAIGTICAGGACAACAGCAITAGTGTCAAGTGGCTGCCTTCAAGTTC 4968	ò 8	5989 CAACCTGCGTTTCCTGGCCACCACCCAATTCCTTGCT
! ≿ £	CCCTGTTACTGGTTACAGAGTAACACCACTCCCAAAAATGGACCAGGACCAACAAAAACTICITTACTTACAGAACAACAACAACAACAAAAACTTCCCAAAAATGGACCAGGACCAACAAAAACAACAAAAAACAACTAAAAAAAA	रंठ व	6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCC
! ≿ £	9 TALAATGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	<i>₹</i> ₹	6109 GGPCCCTCGGCCCCCTGGTGTCACAGAGGCTACTAT
! ≿ £	GTATGTGGTTAGTGTCTATGCTCAGAGGGAGAGAGGTTGCAGCGCTCAGGAGAGGGTTAGTTA	ò q	6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCA
. ≯ ₹	TGCAGTAACCAACATTGATGGCCCTAAAGGCTGGCCATTCACTGGGGGATGCGATTGATT	ठे व	6229 AAGGAAAAAGACAGACGTTCCCCAACTGGTAACCT
i ≽ t	209 CATCAAAATTGCTTGGGAAAGCCCACAGGGGCAAGTTTCCAGGTACAGGGTGACTACTC	∂ 8	6289 ACCAGACATCTTGGATGTTCCTTCCAGGTTCAAAAGAC
R ¥ 8	5269 GAGCCCTGAGGATGCATGAGCTATTCCCTGCACCTGATGAAAAGGATGACCTACTGC 5328 5269 GAGCCCTGAGGAATCCATGAGCTATTCCCTGCACCTGATGATGAAGAAGACACTGC 5328 4921 GAGCCCTGAGGATGGAATCCATGAACTATTCCTTATCCTAACTGATGAAGAAAAAAAA	yo da	6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTC
÷	329 AGAGGTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGT	g 4	6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGAC
! ≿ £	TGATATGGAGAGCCAGCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGA	ò d	6469 CCCCATAAGGCATAGGCCAAGACCATACCGGCGAATGT
! ≿ £	CCTGAAGTTCACTCAGGTCACCACAAGCCTGAGCCCAGTGGACACCACTAGTGT	λ d	6529 GACAACCATCTCATGGGCCCCATTCCAGGACACTTCTGA [
§ ≽ ₽	TCAGCTCACTGGATATCGAGTGGGGGTGACCCCCAAGGAGAGACGGCCCATGAAGA TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAAGACGCGAACAATGAAAGA TCAGCTCACTGGATATCGAGTGGGGGTGACCCCCAAGGAAGACGGACG	& g	6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCC
: ≽ ±	AATCAACCTTGCTCCTGACAGCTCATCGGTGGTTGTATCAGGACTTATGGTGGCCACCAA	ර් සි	6649 TCTGACAGGCCTCACCAGAGGTGCCACTACAACATCAT
; ≽ ;	29 ATATGAAGTGTCTATGCTCTTAAGGACACTTTGACAAGAAGAACAGCAGGAGT 1	<i>₹</i> 0 €	6709 GCAGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGG
? ≿ ≴	TRICACCACTCTGGAGAATGTCAGCCACCAAGAAGGCCTCGTGGACAAGCCAGCTCAGGTGTTGTCAGCCACCTCTGAAAAGGCTCGTGACAAGAAGCTTGATGAAGGCTCGTGACAGATGCTACTGAAGAAGCTCGTGACAGATGCTACTGAAGAAGCTCGTGACAGATGCTAACTGAAGAAGAAGCTCGTGAAGATGCTAACTGAAGAAGAAGAAGAAGAAGAAGAAGAAAAAAAA	<i>₹</i>	6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACAC
2 % %	5749 GACCACCATTAGCTGGAGAAACOTCAACCACCAAAGGGCTGGTGTGTGTACTGA 5400 5749 GACCACCATTAGCTGGAGAACCAAGACTGAGAACGATGATGATGA 5808 6741 GACCACCATTAGCTGGAGAACCAAGACTGAGATGATGATGATGATGATGATGATGATGATGATAGATTGATGA	<i>ò</i> €	6829 AGAIGAGIGGGAACGAAIGICIGAAICAGGCITIAAACT
3 ≱ A	THE CONTROL OF THE CO	₩ da	6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTG

AGAAGAGCGCCCTGATTGG 6228 CTTCCACACCCAATCTTCATGG 6288 ACCACACCGCCACAACGGCCAC 6468 BAGTACATTACATGTCATCC 6588 CCTGGAACTTCTACCAGTGCCAC 6648 CCACTGCCATTGATGCACCATC 5988 ACCCCTTTCGTCACCCACCCTGG 6348 PIGGIAICAIGGCAGCCGCCACG 6048 CTGGGTCTCCTCCAGAGAGT 6108 CTGGTCAGCAACCCAGTGTTGG 6408 ATAGTGGAGCACTGAAAGACCA 6708 AGATCTACCTGTACACCTTGAA 5928 crestarcarescascoscocade s700 credercretechechedadar 5760 ATTACTGGCCTGGAACCGGGAAC 6168 credricadcaaccaardried 6060 STAGGACAAGATCTCTCTCA 6528 sraddadadadcicicica 6180 vragradadecacreaaadacea 6360 GCAACTCTGTCAACGAAGGCTT 6768 ACAGIGICCCATTATGCCGTTGG 6828 INGTIGIGCCAGIGCTIAGGCII 6888 rerrereceaerecriaeerr 6540 GCCATGACAATGGTGTGAACTA 6948

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409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
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TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND TITLE OF INVENTION: USES AND METHODS OF PRODUCING SAME NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,885
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,842
FILING DATE: 21-YAX-1991
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 212-664-0525
TELEFAX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 7705 base pairs
                                                                                                 ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
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Best Local Similarity
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                                                                                                                                                                                                     USA
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STRANDEDNESS:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-826-885-16
                                                                                                                                                                                                COUNTRY:
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                               6601 CAAGATIGGAGAAGAGGACCGTCAGGAAAAATGGCCAGATGATGAGCTGCACATG 6660
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                                                                                                    TCTTGGGAACGGAAAAGGAGAGTTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA 7068
                                                                                                                                                                                                                                                  6721 IGGGAAGACATACCACGTAGGAGAACAGTGGCAGAAGAATATCTCGGTGCCATTTGCTC 6780
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     6949 CAAGATTGGAGAAGTGGGACCGTCAGGGAAAAATGGCCAGATGATGAGCTGCACATG 7008
                                                                                                                                                   6661 TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGTGACCCTCATGAGGCAACGTGTTACGATGA 6720
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Patent No. 5869616
GENERAL INFORMATION:
APPLICANT: VOGE1, Tikva
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Werber, Moshe
Guy, Rachel
Panet, Amos
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Shaked, Hadassa
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US-08-826-885-16
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CGAAAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 588
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                                                          6961 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020
                             7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
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                                                                                                                    CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCCAGCTTAGAGTTCTTC
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0; Mismatches 21; Indels
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APPLICANT: VOGEL, TIKVA; LEVANON, AVIGDOR; WERBER, MOSHE M.; GUY, RACHEL; PANET, AMOS

TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND WETHODS OF PRODUCING SAME

NUMBER OF SEQUENCES: 20

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 526,397
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: 345,952
FILING DATE: 28-APR-1989
APPLICATION NUMBER: 29,951
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Matches 7426; Conservative
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Best Local Similarity 96.3%; Pred. No. 0;
Matches 7515; Conservative 0; Mismatches 15; Indels 273; Gaps
SOFTWARE: Patentin Release #1.0, Version #1.25
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
                                                                                                          FILING DATE: US/07/998,271
                                                                                                                                                                  NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REPRENCE/POCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    7803 base pairs
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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US-08-551-356-1
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                                                                                                                                                                                                                                                                    Query Match
92.7%; Score 7223; DB 5; Length 7803;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 7515; Conservative 0; Mismatches 15; Indels 273; Gaps
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEPHONE: 206-548-2329
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 6..7346
PCT-US93-12687-1
                                                                                                                                                                             TOPOLOGY: linear
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CACAGCCATCTCA CACAGCCATCTCA CACAGAGCAAGCAGCAGCAGCAGCAGCAGAGGAAGCAAGGAAGCAAGAAG		CCACCAGCACCAGCACCTGTGACCAGCACACGTGACAGGAGAGACGACTCCCTTTT	CTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGT	22.9	2281 AGGGAGATGAGCACAGTACCTGGATCTTCCAAGCACCACTTCTGTGAACATCCCTG 2340 2604 ACCTGCTTCCTGGCGGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGC 2663 2341 ACCTGCTTCCTGGCCGAAAATACATTGTAATGTCTATCAGAATATCTAGAGATGGGAAC 2400	AGAGTTTGATCCTGTCTTCACAAACAACAGGGCCTGATGCCCCTCCTGACCGACTG	TGGACCAAGTTGATGCACCCCATATTGTTGTTGGTGGAGCGGAGCCCAGGCTCCCATCA	CAGGGTACAGAATAGTCTATTCGCCATCAAAAGGTAGCAGCAGCAGCAGCACCTTC	CTGAAACTGCAAACTCGCTCACCCTCACGACTTGCACCTGGTGTTCAGTATAACATCACTGAAACTGCAAACTGCATCAGTATTCAGTATAACATCA	CTATCTATGCTGTGGAAGAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGA 	3024 CAGACGTGAAGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACGGCTACCGTG 3083 	29 3084 TGGATGTGATCCCGTCAACCTGGCGGAGGAGGAGGAGGAGGTGCCCATCAGCAGGA 3143	3144 ACACCTTTGCAGAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTG 3203	3204

GACACCATGCGTCACCTGGG 4140

CGTTACTCACCTGTGAAAATG 4190

GACACCATGCGTGTCACCTGGG 4130

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AATGCAGTGGTCTTAACAAATC 4250

aatigcagtigtttaacaaatc gtctacgaacaacatgaggga 4320

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CTCCTCCCACTGACCTGCGATTCACCAACATTGGTCAC 	CTCCACCCCATTGATTTAACCAACTTCCTGGTG	CCACCCCATCCATTGATTTAACCAACTTCCTGGT	AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGAC	494741011101101104745011011001101101100454500110110110110101010	TCCTGCCTGCTACAGAATATGTAGTGAGTGTCTCCAGT	CACCICITAGAGGAAGACAGAAAACAGGICIIGAIICC	accicttagaggaagacagaaaacaggictigatic	ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCT	<u>ratracreccaacrerrracrerececresarrec</u>	ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGA	cadda teedeea tea teedeeda et tead tegaa	ACTCTCGGAATTCCATCACCCTCACCAACCTCACTCCA	cicicosanticalcaccicaccaaccicacic	TCGTTGCTCTTAATGGCAGAGGAAAGTCCCTTATTG	rcgrigcrcrraarggcagaggaaagrccrrarr	CTGATGTTCCGAGGACCTGGAAGTTGTTGCTGCGACC	crdardriccaaddaccrooaagricriccrocaac	GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATC	GGGATGCTCTGTCACAGTGAGATATTACAGGA	ATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAG	Aradoctratocaddadricacrorocorocoadda	TTAAACCTGGAGTTGATTATACCATCACTGTGTATGCT	traaaccreeaetreatraraccarcacrererere	CCGCAAGCAGCAAGCCAATTTCCATTAATTACCGAACA	ccecaagcaaccaartrccarraarraccaa	IGCAAGIGACCGAIGTICAGGACAACAGCAITAGIGIC	TGCAAGTGATGTTCAGGACAACAGCATTAGTGT	1 CTGTTACTGGTTACAGAGTAACCACCACTCCCAAAAAT	TTACTGGTTACAGAGTAACCACCACTCCCAAAAA	1 AAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAA	CTGCAGGTCCAGAACAGAAATGACTATTG	1 AIGIGGITAGIGICTAIGCICAGAAICCAAGCGGAGAG	renggitagrataracicagaarccaagcaag	
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			6411 AACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCACAACGGCCACC 6470	6471 CCATAAGGCATAGGCCAAGACCATACCGGCGAATGTAGGACAAGAAGCTCTCTCT	CAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATCCTG 6	6591 TTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCACTC 6650	6651 TGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGGACTGAAAGACCAGC 6710 	6711 AGAGGCATAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGA 6770 	6771 ACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGGAG 6830 [6831 ATGAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTG 6890	6891 GAAGIGGICATTICAGAIGIGAITCAICTAGAIGGIGCCAIGACAAIGGIGIGAACIACA 6950 	6951 AGATTGGAGAGAAGTGGGACCGTCAGGGAAAATGGCCGGATGAGCTGCACATGTC 7010	7011 TIGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCAIGAGGCAACGTGTTACGAIGAIG 7070 	7071 GGAAGACATACCACGTAGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTCCT 7130 	7131 GCACATGCTTTGGAGGCCAGCGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTG 7190 	7191 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCATC 7250 7201 AACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGATATTCTCAGAGATACCATC 7260	7251 AGAGAACAACAAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACAGG 7310 	7311 CTGACAGAGAATTCCCGAGAGTAAATCATCTTTCCAATCCAGGAAGAAGCATGTCT 7370
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                                                                                                                                                                         Query Match 28.4%; Score 2211.8; DB 2; Length 4027;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 2499; Conservative 0; Mismatches 7; Indels 273; Gaps 1;
                                                                                                                                                                                                                                                       3199 CITTGCAGTGAGCCATGGGAGGGAGGCAAGCCTCTGACTGCTCAACAGACAACCAAACT 3258
                                                                                                                                                                                                                                                                                                                                   3259 GGATGCTCCCACTAACCTCCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATG 3318
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                                                                                                                                                                                                                                                                                             2 CATGGCAGTGAGTCATGGGAGGGAGGAAGCCTCTGACTGCTCAACAAGAACCAAACT 61
LENGTH: 4027 base pairs
                   TYPE: nucleic acid_
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                             ) NAME/KEY: CDS
} LOCATION: 3..4013
US-08-551-356-5
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905	TATAACCGATTCAAGCATCGGCCTGAGGTGGACCCCGCTAAACTCTTCCACCATTATTGG	961
4064		90
962	GTACCGCATCACAGTAGTTGCGGCAGGAGAAGGTATCCCTATTTTTGAAGATTTTGTGTA :	1021
4064		901
1022	CTCCTCAGTAGGATACTACACACACACAGGCCTGGAGCCGGGCATTGACTATGATATCAG	.08
4064	25	901
1082	CGTTATCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAAACAĠĊ	1.4
1142	TGTTCCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCAC	112
4126	TTAACCAACTTCCTGGTGCGTTACTCACTGTGAA 	118
4186	AAATGAGGAAGATGTTGCAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC	424
4 6	TICCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACAGA	4305
30 6	ACACCTCTTAGAGGAAGACAGATCTTGATTCCCCAACTGGCATT	36
1382 4366	CACACCICITAGAGGAGGACACAAAACAGGICIIGAIICCCAACIGGGCAIIGACIIGACAACAAGACACATIIGAATAGAAAACAAGACAACAACAACAACAACAACAACAACAACA	2
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1502	TGGCTACAGGATCCGCCATCATCCGGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGT 	4485
4486	OCATCACCTCACCAACCTCACTCCAGGGGGGGGGGGGGGG	4545
G 6	SCATCGTTGCTCTTAATGGCAGAGGAAAGTCCCTTATTGAT 	4605
Ō	TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGC	99
1682	ricigalgirccaaggaccreaaagirgirecreeaccccaccaccacracr	74
 4666	arigctcctgctctcacagtgacatattacaggatcacttacggaga 	4725
S C	AAATAGCCCTGTCCAGGAGTTCACTGTGCCTGC 	യയ
o o	SCTIABACCIGGAGIIGAIIAIACCAICACIGIAIGCIGICACIGGAG	84
1862	IGGAGTTGATTATCCATCACTGTGTATGCTGTCACTGGCCGTGGAG	92
 1922	SCAGCAAGCCAATTICCAITAATTACC 	4905 1981
 0 6	3ATGCAAGTGACGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAA	96

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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 07//
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 4027 base pairs
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4027 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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                                                           4966 ITCCCCTGTTACTGGTTACAGAGTAACCACCTCCCAAAAATGGACCAGGACCAACAAA
                                                                                                                                      5026 AACTAAAAGTGGAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTGCAGCCCACAGT
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                                                                                                                                                                                                                                                                                                                          2222 GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA
                                                                                                                                                                                                              Sequence 5, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Irani, Meher H.
TILLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
UNMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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3319 GACTCCACCTCGGGCCCCAGATAACAGGATACCGACTGACCGTGGGGCCTTACCCGAAGAGG 3378
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                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
                                                                                                                                                                                                                                                                                                              US 07/998,271
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parker, Gary B
REGISTRATION NUMBER: 31-648
REPERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
OPERATING SYSTEM: PC-DOS/MS-DOS
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4666 CAGCTGGGATGCTCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 4725 1742 CAGCTGGGATGCTCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGG 4725 1742 CAGCTGGGATGCTCTGTGTGTGTGTGTGGAGATCTTACAGCAGAAACAGG 1801 4726 AGGAAATAGCCCTGTCCAGAGTTCACTGTGCTTGGAGCAAGTCTACAGCTACCATCAG 4785	CATTTCCATTAATTACCGAACAGAATT	2042 TTCCCCTGTTACTGGTTACAGAGTAACCACCCCAAAAATGGACCAGGACCAAAAA 2101 5026 AACTAAAACTGCAGGTCCAGAACAACAAATGACTATTGAAGGCTTGCAGCCCACAGT 5085 2102 AACTAAAACTGCAGGTCCAGATCAAACAGAATGACTATTGAAGGCTTGCAGCCCACAGT 2161 5086 GGAGTATGTGGTTAGTGCTAACACAAATCAAATCAAGAGAGAG	GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA GACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGCATTCACTGATGTGGATGTCGA TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGGTGACCTA TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGGTGACCTA TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGGTGACCTA TTCCATCAAAATTGCTTGGGAAAGCCCACAGGGCAAGTTTCCAGGTACAGGTGACCTA		2462 ĠĠĀTĠĀJĀŢĠŖĠĠĠĠĠĠĠĠĠĠŦŢĠĠĀĠĠĠĠĠĠĠĠĠĠĠĠŢŦŢĠĠĀĠĠĠĠĠĠĠĠ	5566 AGRARICARCCTGCTCGTGCTCGTGGTTGTATCAGGACTTATGGTGGCCAC 5625 [
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602 AACAAACTIGCAIGGGAAACCCTGACACTGGAGTGCTCACAGTCTCCTGGGAGAG 661 3859 GAGCACCACCCCAGACATTACTGGTTATAGAATTACCACACACCCTACAAACGGCCAGCA 3918 662 GAGCACCACCCCCAGAACATTACTGGTTATAGAATTACCACACACA	CCCTATCTCTGATACCATCATCCGA	4064 4064 4064 4064 4064 4064 4064 4065	1082 GGTTATCACTCTCATTAATGGCGGCGAGAGTGCCCCTACTACACTGACACAACAACGGC 1141 4066 TGTTCCTCCTCCCACTGACATCACCAACATTGGTCCAACAACAACATCACATGACTCAC 4125 1142 TGTTCCTCCTCCCACTGACTTGACTTCACCACATTGGTCCAGACACATGCGTGTCAC 1201 4126 CTGGGCTCCACCATCCATTGATTTAACCAACATTCCTGGTGCGTTACTCACCTGTGAA 4185 1202 CTGGGCTCCACCCCATCCATTGATTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 1261 1202 CTGGGCTCCACCCCATCCATTGATTAACCAACTTCCTGGTGCGTTACTCACCTGTGAA 1261	AAATGAGGAAGATGTTGCGAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC AAATGAGGAAGATGTTGCGAATTTCTCCTTCAGACAATGCAGTGGTCTTAAC AAATGAGGAAGATGTTGCCAATTTCTCCTTCAGACAATGCAGTGCTTTAAC AAATCTCCTGGCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGA AAATCTCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACAGA GAGCACACCTCTTAGAGGAAGAAAAAAAAAA	GAGCACACCTCTTAGAGGAAGACAGGTCTTGATTCCCCAACTGGCATTGACTT 144 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCACCA (42 TTCTGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 150 TTCTGATATTACTGCCAACTTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCAC 150 TGGCTTACAGATTCGCCACCATCATCCCGAGCACTCACTGGGAACACGGGT 448 TGGCTTACAGGATTCGCCAACACTCAACAGAACCGGGT 156	486 GCCCCACTCTCGGAATTCCATCACCTCACCACCTCACTCCAGGCACAGAGTATGTGGT 4

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4611 CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCT 4670
                                                      1311 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCCAACTGGCATTGACTTTTCTG 4370
                                                                                                                                                                       1371 ATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCT 4430
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                                                                                                                                                                                                                                                                                                                                        368 ACAGGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 427
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                                                                                     248 CACCTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 307
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188 TCCTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCA 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4131 CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAATG 4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4191 AGGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATC 4250
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    CTAGCCCCACTGACCTGCGATTCACCAACATTGGTCCAGACATGCGTGCTGTGTCACTGGG 67

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.0%; Score 1400; DB 4; Length 2481;
Best Local Similarity 76.7%; Pred. No. 0;
Matches 1895; Conservative 0; Mismatches 275; Indels 300; Gaps
                                                                                                                                                                                                                                       Koyana, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshi FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFFCATION: 4Uhrlown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: 4Uhrlown-
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
IS-09-366-009-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 20:
                                                                            Sequence 20, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2481 base pairs
                                                                                                                                                        APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                                   JS-09-366-009-20
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OY 6171 AATATACAATTTATGTCATTGCCTGAAGAATAATCAGAAGGC 2408 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGA OY 6231 GGAAAAGAC 6240 Db 2468 GGAAAAGAC 2477	RESULT 13 US-08-809-156B-20 ; Sequence 20, Application US/08809156B ; Patent No. 6472044	ıto	; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TA TITLE OF INVENTION: CELLS WITH RETROVIRUS ; NUMBER OF SEQUENCES: 39 ; CORRESPONDENCE ADDRESS: ; ADDRESSES: WEIGHER & ASSOCIATES ; STREET: 230 South Fifteenth Street, Suite 500 ; CITY: Philadelphia	COUNTRY: VA ZIP: 19102 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PETER: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30	CARENT APPLICATION DATA: CAPPLICATION NUMBER: FILING DATE: 07-MAR-1997 CLASSIFICATION: 435 FRICR APPLICATION DATA: APPLICATION NUMBER: PCT/JP96/03254	FILING DATE: 07-00V-1996 FILING DATE: 07-00V-1996 FILING DATE: 13-00V-1995 FILING DATE: 13-00V-1995 APPLICATION NUMBER: JP 051847/1996 FILING DATE: 08-MAR-1996	Weiser, Weiser, Wallon N WCE/DOCE UNICATION NCE 215-K: 215-K M FOR SE	SENGTH 2481 base pairs FENGTH 2481 base pairs TYPS: nucleic acid STRANDEDNESS: double FOPOLOGY: linear MOLECULE TYPE: DNA US-08-809-1568-20	Query Match Best Local S Matches 1895 A4071	QY 4131 CICCACCCCATCCATTAACCAACTICTIGGFGCGTTAC
5112AGAATCCAAGCGAGAGAGAGTCAGCCTCTGGTTCAGACTGCAG 5153 1328 AGATCTACTGTACACCTTGAATGACAATGCTGGAGTCCCCTGTGGTCATCGCGCT 1387 5154 TAACCACATTGATGACTCACTACATGCATTCACTGATTCATCATCATTGTGGATTCCATCA 5213		1508 CTGGGTCTCCTCCCGGGGAGTCCTCGGCCCGCGTGGTGGTGGTGGAGAGAGA	TGGAGAGCCAGCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACC	AGCTCACTGGATATCGAGTGGGGTGACCCCCAAGGAGAGGAGCGACCCAATGTTC AGCTCACTGGATATCGAGTGGGGGTGACCCCCAAGGAGAAGAAA AGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAAGAA	TCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAT ATGAAGTGAGTGGTCTTTAAGGACACTTTGACAAGCAGACCGGACTGGCGGAGTTG ATGAAGTGAGTGTCTTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGTTG ATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGCAGCTCAGGGTTTG	5691 TACCACTCTGGAGAATGTCAGCCCACCAAGAAGGCTCGTGACAATGCTGAGA 5750 1928 TCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGCTCGTGTCACAATGCTACTGAGA 5750 5751 CCACCACTCTGCAGAATGTCAGCCCACCAAGAAGGGCTCGTGTCACAGATGCTACTGACA 1987 5751 CCACCACCACTCACCATTAGCTGGAGAACCAAGACTGAGACGACCTGGCCTCCAAGTTGATG 5810 1988 CCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATG 2047			CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCCAGAGAAGTGG	
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GCGAGCCCTGATTGGAA 6230
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|GCGAGCCCTGATTGGAA 2467
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	68 CTCCACCCCATCCATTGATTTAACCAACTTCCTGGTGGGGTTACTCACCTGTGAAAAATG 127 4191 AGGAAGATGTTGCAGATTTGTCACTTCACAATGCAATGC	AGGAAGHTGTTGTGTTGTTGTTGTTTTTTTTTTTGAGACAATGTTGTTTAAGAATTTTTTAAGAATTTTTTAAGAAATTTTTT	4251 TCCTGCCTGGTAACGAATATGTAGTGAGTGACTCCAGTGCTACGAACACATGAGGCA 4310	4311 CACCTCTTAGAGGAAGACAGAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTG 4370 		4431 ACAGATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCC 4490 	4491 ACTCTCGGAATTCCATCACCTCACCAACCTCCAGGCACAGAGATATGTGGTCAGCA 4550		CTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCACCACCTACTGATCAGCTTACTGATCAGCTTGATCAGCTTGATCAGCTTGATCAGCTTGATCAGCTTACTGATCAGCTTACTGATCAGCTTACTAGCTACCACCACCACCACCACCACCACCACCACCACCACCAC	GGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAGAACAGGAAA	SCGATGCTCCTGCTGCTCAGTGAGGTATATTACAGGAGTCACTTACGGAGAAAACAGGAGGAAATAGGAGGAAGTCTACAGCAGGAGGCCCCTGGGGAGGAAGTCTACAGCTACAGCAGGCCCCTTACAGCTACAGCAGCAAGTCTACAGCTACAGATCAAGCAGCAGCCCTTACAGCTACAGCTAAAAAAAA	TIAAACTIGGAGIIGATIAIACAICAGGGGGGAGGGGGGGGGG	CCGCAAGCAGGAAGCCAATTTCCATTAATTACCGAACAGAATTGACAAGCCATCC		TCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACAAAAAAAA	ATGGACCAGGACCAACAAAACTACAGGTCCAGGTCCAAGGACCCCCAAGGAATGGACCCAAGGAAATGACTGCAGGACCCAGGAAATGACTATTG	AGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTAT AAGGCTTGCAGCCCAGTGGAATATGTGGTTAATGTCTC	1028 CAGGACTTATGGTGGCCACCAAATATGAAGTGAGTGTGTTATGCTCTTAAGGACACTTTGA 1087	1088 CAAGCAGCCACGCTCAGGGTGTTGTCACCACTCTGGAGAATGTCAGCCCCCCCAAGAAGGG 1147

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                    2288 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGG 2347
                                                                   6111 TCCCTCGGCCCCGCCCTGGTGTCACAGAGCTACTATTACTGGCCTGGAACCGGGAACCG 6170
6051 CCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCTCCCAGAGAAGTGG 6110
                                                                                                     2348 TCCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCG 2407
                                                                                                                                       6171 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGGGGGGCCCCTGATTGGAA 6230
                                                                                                                                                                       2408 AATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGGGCCCTGATTGGAA 2467
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 02-049-1999
CLASSIFICATION: <UNKNOWT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: 4UNKNOWN-
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: UP 051847/1996
FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
ELEBENDRE: 215-85-833
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1722 base pairs
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 39
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US-09-366-009-33
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Best Local Similarity 79.5%; Pred. No. 2.1e-253; Matches 1130; Conservative 0; Mismatches 283; Indels
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1317 GTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCAT 1376
                                    5977 TGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCAATTCCTTGCTGGTATCATG 6036
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                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
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APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
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FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
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APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Uemo, Takashi
APPLICANT: Koyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6472204
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REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                            11.8%; Score 921.2; DB 4; Length 1722;
79.5%; Pred. No. 2.1e-253;
tive 0; Mismatches 283; Indels 9; Gaps
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1722 base pairs
; TYPE: nucletc acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-809-156B-33
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1130; Conservative
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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6097 TCCCAGAGAAGTGGTCCCTCGGCCCCTCGGTGTCACAGAGGCTACTATACTGGCCT 6156
1497 TCCCAGAGAAGTGGTCCTCGGCCCCGCCCTGGTGTCACAGAGGCTACTATACTGGCCT 1556
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1317 GTACACCTTGAATGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCAT 1376
                                                                                                                                                                                                                                                                             5977 TGATGCACCATCCCAACCTGCGTTTCCTGGCCACCACCCAATTCCTTGCTGGTATCATG 6036
1377 TGATGCACCATCCAACCTGCGTTTCCTGGCACCACCAATTCCTTGCTGGTATCATG 1436
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5797 CCTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCC 5856
1197 CTTCCAAGTTGATGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGGC 1256
                                                                                                                       1257 AGATGTCAGAAGCTACACCATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCT 1316
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Search completed: March 7, 2004, 21:48:28 Job time : 595 secs

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GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

March 7, 2004, 05:41:46 ; Search time 2538 Seconds

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3373863 seqs, 2124099041 residues earched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	escription	Aas94866 Human DNA	Aai57805 Human pol	1804 Human	Aai57802 Human pol	Adb31322 Testoster	37	Aba82689 Fibronect	0	N	Abz96825 Human nuc	Acf03878 Human fib	Abx10391 DNA encod	Acc46009 Human fib	Acf12859 Human cer	Aca64817 Human fib	Aca64819 Human fib	Adb70377 Fibronect	Adb98703 Human fib	Add18771 Human dis	Ade82499 Human DNA	Aaa35010 Human ade	Aaf21132 Human low	Abz96826 Human nuc
COLUMN TO THE PERSON OF THE PE	ID	AAS94866	AA157805	AAI57804	AA157802	ADB31322	AAF21131	ABA82689	ABL67540	ABT11082	AB296825	ACF03878	ABX10391	ACC46009	ACF12859	ACA64817	ACA64819	ADB70377	ADB98703	ADD18771	ADE82499	AAA35010	AAF21132	ABZ96826
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ALIGNMENTS

Human DNA sequence #121 expressed during foam cell differentiation. Human, foam cell differentiation, atherosclerosis, cerebral stroke, cardiovascular disorder, coronary artery disease, gene therapy, ds. AAS94866 standard; DNA; 8044 BP. 04-APR-2001; 2001WO-US011128. 05-APR-2000; 2000US-0195106P. (INCY-) INCYTE GENOMICS INC. 14-FEB-2002 (first entry) WO200177389-A2. Homo sapiens. 18-OCT-2001. AAS94866; rai J; RESULT 1 AAS94866

Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T; WPI; 2002-010925/01.

Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.

Claim 1; Page 175-177; 315pp; English.

The present invention relates to the isolation of human polymucleotide sequences that are differentially expressed during foam cell differentiation. The polymucleotide sequences of the invention or a composition comprising these polymucleotides are useful as a high throughput method for detecting altered expression of one or more polymucleotides in a sample. The polymucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polymucleotide sequences can also be used as PCR primers and probes. The polymucleotides of the invention are also

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useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
                                                                                               Query Match 99.8%; Score 7780.6; DB 6; Length 8044; Best Local Similarity 99.9%; Pred. No. 0; Marches 7786; Conservative 0; Mismatches 9; Indels 0;
                                                                  Seguence 8044 BP; 2143 A; 2107 C; 1977 G; 1817 T; 0 U; 0 Other;
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5521 ATATCGAGTGCGGGTGACCCCCAAGGACGGACCAATGAAAGAATCAACCTTGC 5580 5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGGGTTGCCTTGCACGATGATATGGAGAG 5400 5341 CCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGATGATGAGAG 5400 5401 CCAGCCCTGATTGGAACCCAGTCCACTATTCCTGCACCAACTGACCTGAAGTTCAC 5460 5401 CCAGCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCAC 5460 5461 TCAGGTCACACGCACAAGCCTGAGGGCCCAGTGGACACCACCAATGTTCAGCTCACTGG 5520 5461 TCAGGTCACACCCACAAGCCTGAGCGCCCAGTGGACACCACCCAATGTTCAGCTCACTGG 5520 5581 TCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAAATATGAAGTGAG 5640 5581 recreacedercareceregriciareaggaerraregregeeaceaeaarargaagreag 5640 5641 IGICTATGCTCTTAAGGACACTTTGACAAGCAGACCAGGCTCAGGGAGTTGTCACCACTCT 5700 5641 TGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGTGTTGTCACCACTCT 5700 5701 GGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760 5701 GGAGAATGTCAGCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGAGACCACCATCAC 5760 5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGATGCCGTTCCAGC 5820 5761 CATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCCGTTCCAGC 5820 5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880 5821 CAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAGCTACACCATCAC 5880 5881 IGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACCTTGAATGACAATGCTCG 5940 5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000 5941 GAGCTCCCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTT 6000 6001 CCTGGCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTAC 6060 6001 CCTGGCCACCACCCAATTCCTTGCTGGTATCATGGCAGCCGCCAGGTGCCAGGATTAC 6060 6061 CGGCTACATCAACAATAAGAAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120 6061 CGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCC 6120 6121 CCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGGAACCGAATATACAAT 6180 6121 ccgcccrosrcrcacagacscracrarracrosccrosaaccggaaccgaararacaar 6180 TIAIGTCATIGCCCTGAAGAATAAICAGAAGAGCGAGCCCCTGAITGGAAGGAAAAAGAC 6240 6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCCAATCTTCATGGACCAGAGATCTT 6300 6241 AGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGGACCAGAGATCTT 6300 6301 GGATGTTCCTTCCACAGTTCAAAAGACCCCTTTCGTCACCCCACCCTGGGTATGACACTGG 6360 6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGGGCAACAAATGAT 6420 6361 AAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCAGTGTTGGGCAACAAATGAT 6420

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ), nootropic; immunosuppressant; cytostatic; gene therapy; cancer; heral nervous system; CNS; immer's; Parkinson's disease; Huntington's disease; haemostatic; rophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; kinetic; thrombolytic; drug screening; arthritis; inflammation; emia; ss.
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PAN-2000; 2000US-00488725.
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UL-2000; 2000US-00620312.
UG-2000; 2000US-00653450.
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UGT-2000; 2000US-00653450.
UGT-2000; 2000US-00593036.
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of the invention may be used to treat diseases of the peripheral nervous 8888888888888888

a injuries, peripheral neuropal as injuries, peripheral neuropal nervous system diseases, sur Huntington's disease, amyotro Syndrome. Other uses include h as: Immune system suppressictic/chemokinetic activity, h diagnosis and inflammation, leuk ce data for this patent did no other	Similarity 99.7%; Score 7774.8; DB 4; Len 99.7%; Score 7774.8; DB 4; Len 9; Conservative 0; Mismatches 7; Inde	10 CCGGCTGTGCTGCACAGGGGAGGGAACCCCAGGCGGAGGGGAGGGGACC 69	70 TGCAGCCACAACTTCTCTGGTCCTCTGCATCCCTTCTGTCCCTCCACCGGTCCCCTTCCC 12	130 CACCTCTGGCCCCCACCTTCTTGGAGGCGACAACCCCCGGGGGGGTTTGGAGGGATTT 189	190 TICCCGCAGGTTGCGAAGGAAACCTTGGTGGCAACTTGCTCCCGGTGCGGGGTT 249	250 TCTCCCCACCGTCTCAACATGCTTAGGGGTCCGGGGCTGCTGCTGCTGCTGGCCGT 309	310 CCTGTGCCTGGGGACAGCGGTGCCCTCCACGGGAGCCTCGAAGAGGAAGAGGCAGGC	370 GCAAAIGGTICAGCCCCAGICCCCGGIGGCIGTCAGICAAAGCAAGCCCGGIIGITAIGA 429 	430 CAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCT	490 GGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGAAAGTAAACCTGAAGCTGA 549 	550 AGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTGGCTGACACTTATGAGCG 609	610 TCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGGTGGGGGGGG	670 CTGTACCATGGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAAGATTGGTGACACCTG 729	4 – 4 8 8 8 8	90 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGCTGGGACTTC 84	884 AGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATGCTGGGGACTTC 943
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			chemokinetic; thrombleukaemia; ss. Homo sapiens. WO200153312-A1. 26-UUL-2001. 26-DEC-2000; 2000WO-23-DEC-1999; 99US-
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous solution is peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic clateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemorectic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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Best Local Similarity 98.7%; Pred. No. 0;
Matches 7779; Conservative 0; Mismatches 7; Indels 93;
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                                  Claim 1, SEQ ID NO 7, 10078pp; English.
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6190 TGCCCTGAAGAATAATCAGAAGAGCCAGCCCTGATTGGAAGGAA	6524 ÀCATGGTTTTÀGGGGÀCGACACGACACAGGCCACCATAAGGCATAGGCATAGGCATAGGCCAAG 6583 6490 ACCATACCCGCCGAATGT	6914 CAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCA 6816 6914 CAACGAAGGCTTGAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCA 7003 6817 TTATGCCGTTGGAACCAACCTACGGATGACTCGTGCTTTGACCCCTACAGTTTCCCA 7003 6817 TTATGCCGTTGGAGTGGGACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCA 7063 6817 TTATGCCGTTGGAGTGGGTGCGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCA 7063 6817 TGGCTTAGGCTTTGGAAGTGGGAACGAATGTCTGAATCAGGCTTTAAACTGTTGTGCCA 7063 6817 TGGCTTAGGCTTTGGAAGTGGAACGAATGTCTGAATCATCAGATGACAA 6936 7064 GTGCTTAGGCTTTTGGAAGTGGTCATTTCAGATGTTCATCAGATGATCAGATGACAA 6936 7124 GTGCTTAGGCTTTTGGAAGTGGTCATTTCAGATGTTCATCAGATGATCAGATGACAACTGAGGAACTGAAGTGATTCAAGTGGTCAGAAATTGGAGGAAGTGGATTCAGATGATGAAATTGAGGAAAATTCAAGTGTGAAAATGGCCAGATGAT 7183 6997 GAGCTGCAACATTGGAAGAAAAGAGAAATTCAAGTGTGACCCTCATGAGGCAAC 7243 7057 GTGTTACGATTGGAAGAAAAGAGAAATTCAAGTGTGACCCTCATGAGGAAACTCCG 7116 7117 TGCCATTTGCTCCTGCACATTTGGAAGAAAAAGAGAAATTCAAGTGTGACAAACTGCG 7166 7117 CGCATTTGCTCCTGCACATTTGGAAGCCAGAGAAAATGGCCAGAAAATTCCCG 7166 7117 CGCATTTGCTCCTGCACATTGGAAGACCAGAGGAATATCCCG 7166 7117 CAGACCTGGGGGTGAACCCAGTACGCAGAGCCAGAGGAATATCCCG 7166 7117 CAGACCTGGGGGGTGAACCCAGTACGCGGGGCTGGCGCTGTGACAACTGCCG 7166 7117 CAGACCTGGGGGTGAACCCAGTACCAGTACCCAGAGCCTGTGACAACTGCCG 7166 7117 CAGACCTGGGGGGTGAACCCAGTACCCAGAGGCCTGGCGCTGTGACAACTGCCG 7166 7117 CAGACCTGGGGGGTGAACCCCAGTACCCAGAGCCAGACCTGCCGCTGTGCCCTTACAACTGCCG 7166 7117 CAGACCTGGGGGGTGAACCCCAGAAGGCCACACTACTGGCCCTGACCAGTACCTGCCGTACACTGCCGTGCCCTTACAACTGCCCTACAGTACTCCTTTTGAAGCCCTGCCGGGGCTGTGCCTGTACAACTGCCTGC

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeprides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotacis/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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Zhao QA;
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Zhang J,
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97.7%; Score 7614.8; DB 4; Length 8062;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 7704; Conservative 0; Mismatches 7; Indels 75;
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Yang Y,
                                                                                                                                                Liu C, Asundi V, Chen R, Ma Y, (Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                         central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      part of the printed specification
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653911.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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GTACACCTTGAATGACAATGCTGGAGCTCCCC 5949 TGCACCAACTGACCTGAAGTTCACTCAGGTCAC 5469 ACCACCCAATGTTCAGCTCACTGGATATCGAGT 5623 ACCAATGAAAGAAATCAACCTTGCTCCTGACAG 5589 GGTGGCCACCAATATGAAGTGAGTGTCTATGC 5649 egigeccaccaatarcaacrdacrdrcrargc 5743 AGCTCAGGGAGTTGTCACCACTCTGGAGAATGT 5803 AGAIGCIACIGAGACCACCAICACCAIIAGCIG 5769 AGATGTCAGAAGCTACACCATCACTGGCTTACA 5889 AGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5443 TGCCTTGCACGATGATATGGAGAGCCAGCCCT 5503 ACCACCCAATGITCAGCTCACTGGATATCGAGT 5529 AGCICAGGGAGIIGICACCACTCTGGAGAAIGI 5709 CAAACCATCCCAGATGCAAGTGACCGATGTTCA 4929 ACCAACAAAAACTAAAACTGCAGGTCCAGATCA 5143 TCTGGTTCAGACTGCAGTAACCAACATTGATCG 5169 GGATGTCGATTCCATCAAATTGCTTGGGAAAG 5229 GGATGTCGATTCCATCAAATTGCTTGGGAAG 5323 GGTGACCTACTCGAGCCCTGAGGATGGAATCCA 5289 AGAAGACACTGCAGAGCTGCAAGGCCTCAGACC 5349 TGCCTTGCACGATGATATGGAGAGCCAGCCCCT 5409 GCCTTCAAGTTCCCCTGTTACTGGTTACAGAGT 4989 ACCAACAAAACTAAAACTGCAGGTCCAGATCA 5049 GCCCACAGTGGAGTATGTGGTTAGTGTCTATGC 5109 decedecadadadrarendariadrendaren 5203

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24-DEC-1997;

98US-0079303P. 97US-0068821P. (MILL-) MILLENNIUM PHARM INC WPI; 2003-595981/56. 25-MAR-1998;

Determination of whether compound is useful for prostate cancer treatment comprises measuring expression level of specific nucleic acid sequence in prostate cancer cell sample in the presence and absence of compound.

Example 1; Col 139-146; 194pp; English.

The invention discloses a method for determining whether a compound can be used to treat prostate cancer and comprises measuring the expression level of a mucleic acid in prostate cancer cell sample in the presence and absence of the compound. Determining whether a compound can be used to treat prostate cancer comprises identifying the compound as useful for prostate cancer treatment when the expression level of the nucleic acid in the presence of the compound. State cancer is usually tretaed by androgen withdrawal, by castration or through the use of an anti-androgenic drug. Bicalutamide (casodex) is one such anti-androgenic compound. The determination whether a selected compound, e.g. an anti-androgenic compound or testosterone, can be used to treat the prostate cancer can be made on a patient by patient basis. The sequence presented is a gene which is more highly expressed in testosterone treated prostate

Sequence 7679 BP; 2081 A; 1981 C; 1862 G; 1755 T; 0 U; 0 Other;

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oligonucleotides the A is replaced by a 'Universal' or alternative base.

(1) can have respiratory, bronchodilator, antinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and malignancies, such as stimulating and activating peptide factors and malignancies, such as stimulating and chemokines endogenously produced specific and non-specific enzymes, chemokine receptors, adension molecules and then specific enzymes, binding proteins, adension molecules and non-nervous system (CNS) and peripheral nervous and non-nervous system creeptors, defensine, growth factors, bradykinin receptors, central nervous soften peptide transmitters, defensine, growth factors, vasociated proteins. The antisense olisonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or condition especial washers or including especial or not adlesses or condition especial. condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS); pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

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Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

648 480 768 541 crocardardoradarrorractrocerdodadadecadedadedarederredaetre 600 468 588 708 301 gecreseceadesadaraadereratecarcecaadececreseareadedegecateade 420 TGTGTGTCTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAAAGTGTTT 828 CTGGATGATGGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTC 948 61 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 120 GACCTACCTAGGTAATGTGTTTGTACTTGTATGGAGGAAGCCGAGGTTTTAACTG 180 AGTGGGTGACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300 9 409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG CGAAAGTAAACCTGAAGCTGAAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 649 GGCTGGGCGAGGGAGTATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 361 cracaagarregreacaccresassasccacareassacresregrearracarerrasasre rereretratagaaaaagaagaargacerecaagecearagererer 829 TGATCATGCTGCGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCTTACCAAGG 181 cgaaagraaaccrgaagcrgaagagcrrgcrrrgacaagracacrgggaacacrracc 0; Gaps 95.2%; Score 7423; DB 3; Length 7680; 99.8%; Pred. No. 0; tive 0; Mismatches 15; Indels 0 Best Local Similarity 99.8 Matches 7432; Conservative 469 121 589 241 709 169 421 Query Match 원 ò 셤 ö d ద ઠે g à 심 ò d ò В ò 셤 ò ઠે ð

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	GGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC GGCACTGATGAAGAACTCTTACAGTTTTACTGGAACTTCTACCAGTGCCAC ACAGGCCTCACCAGGAGGTGCCTACAGAGGTGAAAGATGAAGGCACAACATCATAGAAGGCAACATCAAAAGAACATCATAAAAGAGAAGAACATCATAATGAAAGACATCATAAAGAGAAGAACATCATAAAGAGAAGAACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAACATCATAAAAGACATCATAAAAGACATCATAAAAGACATCATAAAACATCATAAAACATCATAAAACATCATAAAACATCAT	PAPE TELE	CAGTGCT CAGTGCT	acaatggtgt acaatggtgt	CAGCGAGAAATGGCCAGATGATGATGAGCTGCA 	aagtotgaccctcatgaggcaacgtottac 	CACGTAGGAGAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGC 	CAGCGGGGCTGGCGCTGTGACTGCCGCAGACTGGGGGG 	CCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA	GITAAITGCCCAAITGAGIGCTTCAIGCCTTTAGAIGTACA 	ccagaggaacaag ccagaggaacaag	CCATCTAAACTIGGAGTGATGTTAGCAGACCCAGCTTAGAGTTC 	<u>8</u> _8
6061	6589 TGTTGGCACTGATGAAGAAC 6241 []	09 GCAGAGGCATAA 	829 AGAT 481 AGAT	6889 IGGAAGIGGICATITCAGA 	6949 CAAGATTGGAGAGAAGTGGGACCGT 	7009 TCTTGGGAACGGAAAAGGAGAATTC 	7069 TGGGAAGACATACCACGTA(7129 CTGCACATGCTTTGGAGGCC	7189 TGAACCCAGTCCCGAAGGC 	7249 TCAGAGAACAAACACTAATG	7309 GGCTGACAGAGAAGATTCC 	7369 CTCTCTGCCAAGATCCATC	7429 TITCITICITAAGCCCTITG

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                                                                                                                                            CIGGCCCCCAAIACIGIAGGAACAAGCAIGAICIIGIIACIGIGAIAIIIIAAAIAICCA 7788
                7141 rerecaaceareacereseasarrrecteasesrrrectaraareaseserecarr 7200
                                                7549 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
                                                                                7201 GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260
                                                                                                                   TITGGITTIGGGATCAATAGGAAAGCATATGCAGCCAACCAAGATGCAAATGTTTTGAAAT 7668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; high bone mass; HBM gene; Zmaxi gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis; osteomalacia; fibrous dysplasia; ds.
New high bone mass (HBM) and Zmaxl genes and proteins useful for modulating bone mass for the treatment of \varepsilon.\,g. osteoporosis.
                                                                                                                                                                                     7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carulli JP, Little RD, Recker RR, Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 79; Page 376-378; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA82689 standard; DNA; 7680 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibronectin gene SEQ ID NO:75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2000; 2000WO-US016951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000; 2000US-00543371.
05-APR-2000; 2000US-00544398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                         7789 CAGTACT 7795
                                                                                                                                                                                                                                                                                                                                                         7441 CAGTACT 7447
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Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

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95.2%; Score 7423; DB 5; Length 7680;

1021 TGGCAGGACGTTCTACTCCTGCACACAGGAACTACACACAC	2269 CATCAAAGGCCTGAAGCCTGGTGTATACGAGGGCCAGCTCATC 1921 CATCAAAGGCCTGAAGCCTGGTGTGTGTTACGAGGGCCAGCTCATC 2329 CGGCCACCAAGAAGTGACTGGCTTTGACTTCACCACCAGCACC 1981 CGGCCACCAGAAGTGACTGGCTTTGACTTCACCACCAGCACC 2389 CAGCAACACGTGACAGGAGAGAGACACCTCTCACCACCAGCACC 2389 CAGCAACACGTGACAGAGAGAGAGACACCCTTTTCTCCTCTTTGTG 2341 CAGCAACACCGTGACAGAGAGAGACACCCCTTTTTTTTTT
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1008 1128 1120 120 120 120 120 120 120 120 128 120 120 120 130 130 130 130 130 130 130 130 130 13	840 1248 900 1308 1368 1428
inilarity 99.8%; Pred. No. 0; Insert ches 15; Indels 0; Gaps Conservative 0; Mismatches 15; Indels 0; Gaps Gardactavative 0; Mismatches 15; Indels 0; Gaps Gardactartive 0; Mismatches 15; Indels 0; Gaps Gardactartive 0; Mismatches 15; Indels 0; Gaps Gardactartive 0; Mismatches 15; Indels 0; Gaps Gardactartive 0; Mismatches 0; Mismatches 0; Gardactartive 0; Mismatches 0; Management 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Management 0; Mismatches 0; Mismatch	CCCCAGCCTCACCCCCAGCCTCCTCCCTATGGCCA TRATTCTGTGGGGATGCAGTGGAAGACACAAGG TTGGGCAACGGATGCAGTGGAAGACACAAGG TTGGGCAACGGATGCAGTGGAAGACACAAGG TTGGGCAACGGATGCAGTGGAAGACACACTGTGGCAAGGCAAGGGATGCTTACCATTCACTTACAAAAAAGAAGAAGTGTGTTACATTCACTACAAAAAGAAGAAGAAGAAAAAAAA
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CAGCACACCTGTGAC 2040 CAGCTTCCGACACCGT 2508 ACTTAAACTCCTACAC 2268 CCAGCACCTGTGAC 2388 ACTGIACAIGCIICGG 1908 AGGATTCAGAGACTGG 1968 HILLIHILIHIH HIR TACAGACCTATCCAAG 2088 AGCCCAACTCCCACCC 2148 TTCTCAGGTGGAGACC 2208 FICTCAGGTGGAGACC 1860 PCAGCATCCAGCAGTA 2328 REGCCACTTCTGAATC 2448 ATCAGTGGGATAAGCA 1380 STCGTGGGGATGGAC 1440 ACTGTACATGCTTCGG 1560 STGTCAGATACCAGTG 2028 ACATCTTTGGTGCAG 1080 cargaagregrereg 1608 CATGGCTGCCCACGA 1668 TCAGTGGGATAAGCA 1728 STCGTGGGGAATGGAC 1788 ACATCACTTACAATGT 1848 AGACCACACTGTTT 1488

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acgaccaagccagggaggaggggc 	retercceectigactccaegagt 	acaggaagagatgcgccaattgt 	rtigcatctggaggcaaaccctga 	DACCCCAGACATTACTGGTTATAG 	rictitiggaagaagtggiccatge 	cggcctggagtacaatgtcagtg1 	CTCTGATACCATCCCCAGCTG1 	rccagacaccargegrgrcaccr(ogtgcgttactcacctgtgaaaa 	agacaatgcagtggtcttaacaai 	CAGTGTCTACGAACAACATGAGAK 	TTCCCCAACTGGCATTGACTTTT(TGCTCCTCGAGCCACCATCACTG(GAGACCTCGAGAAGATCGGGTGO 	TCCAGGCACAGAGTATGTGGTCA 	ATTGATTGGCCAACAATCAACGG 	GACCCCACCAGCCTACTGATCA 	GATCACTTACGGAGAAACAGGAG
CTCCAAGAATTGGTTTTAAGCTGGGTGTZ 	aagtgacttcagactcaggaagcatcgt 	TCTACACCATCCAAGTCCTGAGAGATGGF 	TIGGTGACACCATTGTCTCCACCAACAAA 	TIGCTCACAGTCTCCTGGGAGAGGAGGAGCACC 	CAACCCTACAAACGGCCAGCAGGGAAF. 	GCTCCTGCACTTTTGATAACCTGAGTCCC 	itcaaggatgacaaggaaagtgtccttat(069 TCCTCCTCCACTGACTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTG 4128	CCCCATCCATTGATTTAACCAACTTCCT(angitigcagagitgicaatitciccitgi 	CTGGTACAGAATATGTAGTGAGTGTCTC 	titagaggaagacagaaaacaggictiga 	ACTGCCAACTCTTTACTGTGCACTGGAT	ATCCGCCATCATCCCGAGCACTTCAGTGG 	CGGAATTCCATCACCTCACCAACTCAC 	GCTCTTAATGGCAGAGGAAGGAAAGTCCCTT 	gitcgaggactiggaagitgitgicgc 	GCTCCTGCTGTCACAGTGAGATATTACAG
GACGCCTG GACGCCTG	ACCACGAG ACCACGAG	agaatacg 	AAACAAAG AAACAAAG	CACTGGAG CACTGGAG	AATTACCA AATTACCA	TGATCAGA TGATCAGA	TTACACTO TTACACTO	TCCTCCTC	GGCTCCAC	TGAGGAAC TGAGGAAC	1010010 	CACACCTC CACACCTC CACACCTC	TGATATT/ TGATATT/	CTACAGG	CCACTCT 	CATCGTT CATCGTT	TTCTGAT	CTGGGAT
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7321 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380
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6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGCTGCCATGACAATGGTGTGAACTA 6948
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                               Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid,
stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
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          Thyroid cancer related gene sequence SEQ ID NO:5877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 5877; 44pp; English.
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25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235924P.
25-SEP-2000; 2000US-023503P.
25-SEP-2000; 2000US-023503P.
25-SEP-2000; 2000US-0235384P.
25-SEP-2000; 2000US-0235384P.
25-SEP-2000; 2000US-0235380P.
27-SEP-2000; 2000US-023538P.
27-SEP-2000; 2000US-0235884DP.
27-SEP-2000; 2000US-0235884DP.
27-SEP-2000; 2000US-0235884P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023603P.
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03-0CT-2000; 2000US-0237425P.
03-0CT-2000; 2000US-0237504P.
03-0CT-2000; 2000US-0237504P.
03-0CT-2000; 2000US-0237604P.
01-NOV-2000; 2000US-024867P.
01-NOV-2000; 2000US-024867P.
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                                                                                   gene; ds.
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The present invention describes a method (MI) for screening for an anti-

ABL67540 standard; DNA; 7680 BP.

15-MAY-2002 (first entry)

ABL67540;

ABL67540 ID ABL6 XX AC ABL6 XX 15-N

RESULT 8

us-10-084-817-2.rng

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coppastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous call carcinoma, neutroendocrine carcinoma, papillary carcinoma and Wilm's
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Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other; 888888888888888888888

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,	6; 15;	CCCAGT	ATCAG	ATCAG	ATGGA	ATGGA	ACAAG	ACAAG	TGATC	TGATO	ACCGC	ACCGC	AGACT	AGACT	GCAAG	GCAAG	BAAACG	PARACO	SCAGO	GCAGO	CCTAT	CCTAT	TCTGC	ATCTGG	ACATCO
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	re 7423; d. No. 0; Mismatche	ATGGT	GGAAA	GGAAA	TGTAC	TGTAC	ACTTG	ACTTG	AAAGA	AAAG	GTACCATCGCAAACCG	ACCA	BAGACC	SAGACC	AGAATO	AGAATO	GTGG	rgrag	CTGG	CCTGGC	CACAAC	CACAAC	GCTCC	30100	rgrac.
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3	95 99 it iv	AGGCA	GGTTG	1000 1000 1000 1000 1000 1000 1000 100	GGCA	GGTAZ	CCTG	CCTG	ACTI	ACTTA	AGGGAC	AGGGAC	rggrg.	rgGTG	rggTA.	GGTA	FGCTG	rgctg	SGTAG	GTAG	ATGCA	ATGCA	TAATO	TAATO	TGAGA
4	larity Conserva	GAAGAGCAAGAGGCAGGCT 	AGCCC	AGCCC	TACCTA	ACCTA	GTAAZ	GTAA	GTGAC	GTGAC	3GGCG/	19295 19395	AAGAT	AGAT.	FGTCT	GTCT	CATGC	CATGC	ATGAT	ATGAT	AATAG	AATAG	AAGGA	AAGGA	AAGTG
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1129	CGATGITCGTGCAGCTGITTACCAACCGCAGCCTCACCCCCAGCCTCCTATGGCCA 1188
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1249	AAATAAGCAAATGCTTTGCAOGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGTGT 1308
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1489	GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAA 15.
1549	CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGACAACAACATGAAGTGGTGTGG 160
1609	GACCACACACAAAATATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 166
	ggraficecacaccartgragggtcatgtrccgcattggagatcagtgggataagga
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2029	9 CTACTIGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACACACCTATCCAAG 2088
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5881 AAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCTTCCACACCCAATCTTCATGG 5940 6121 ccccaraaggecaraggeccaagaccaracceccgaargraggacaagaagcrecrerere 6180 6529 GACAACCATCTCATGGGCCCCCATTCCAGGACACTTCTGAGTACATCATTTCATGTCATGC 6588 5341 iercaccacreredadadreredececaccadadadeceredadadadadadadareeracida 5400 5401 GACCACCATCACCATTAGCTGGAGAACCAAGACGATGAGAGGATCACTGGCTTCCAAGTTGA 5460 5809 TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG 5868 5461 IGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAACCATCAAGCCAGATGTCAGAAG 5520 5521 cracaccarcacaderrracaaccadecacaderracaadarcraccidracaccrraaa 5580 5929 TGACAATGCTCGGAGCTCCCCTGTGGGTCATCGACGCCTCCACTGCCATTGATGCACCATC 5988 ssel reacaargercegagerecerererefereredecerecerecaerecarrearecaeeare 5989 CAACCTGCGTTTCCTGGCCACCACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACG 6048 s641 caaccrecerriceresceaceceaceacrecerricerriserareareaceaceaceaceace 5701 reccadearraccederacarcarcardadrareaderaccredericrecredeadader 5760 6109 GOTCCCTCGGCCCCCGGCCTGACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 6168 5761 edrocorodeccoedecoroderarchehadadecorhorratianadosecorodenadosedade 5820 6169 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGGGGGCCCTGATTGG 6228 5821 CGAATATACAATTTATGTCATTGCCCTGAAGAATAATCAGAAGAGCGGAGCCCCTGATTGG 5880 6229 AAGGAAAAAGACAGACGTTCCCCAACTGGTAACCCTTCCACACCCCAATCTTCATGG 6288 5629 ATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGCAGACCCAGCTCAGGAGT 5688 5749 GACCACCATCACCATTAGCTGGAGGAACCAAGACTGAGACGATCACTGGCCTCCAAGTTGA 5808 5869 CTACACCATCACTGGCTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAA 5928 5101 CCTGAAGTTCACTCAGGTCACACACAAGCCTGAGCGCCCAGTGGACACCACCAATGT 5160 5161 reascreacrasararesagracissorsacececaasaaaaaacecaaraaaaaa 5220 5509 TCAGCTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCGGACCAATGAAAGA 5568 5569 AATCAACCTTGCTCCTGACAGCTCATCCGTGGTTGTATCAGGACTTATGGTGGCCACCAA 5628 6061 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACGCCCCACAACGGCCAC 6349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTAGCAACCCAGTGTTGG 6001 Grangacacregaaaregrarreagerrecregeaerreregreaecaecaeceaerres 6409 GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACGCCCACAACGGCCAC 6469 CCCCATAAGGCCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCA 6049 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGT 5689 TGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATGCTACTGA 임 g g δ 셤 ઠે 8 엄 엄 ò ð g $\overset{\circ}{\delta}$ ద g 엄 ें g ठ ઠે ò ద ò 셤 ò a ઠે 셤 à 임 à ઠે 엄 ઠે ઠે CCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGGGCCCAGTGGACACCACCAATGT 5508 4860 TGATATTACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTGGAGCCACCATCACTGG 4080 TTCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAG 4668 GATGCAAGTGACCGATGTTCAGGACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTC 4968

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9 IGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC	9 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGACTGAAAGACCACTAAAGACCACTACAAAGACCACTACAAAGACCACTACAAGACCACTAAAAGACCACTAAAAGACCAACATCATAGTGGAGGGACTGAAAGACCA	9 GCAGAGGCATAAGGITCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 	9 GAACCAACCTAOGGATGACTGGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG 	9 AGATGAGTGAGGAACGAATGTCTGAATCAGGCTTTAAA.CTGTTGTGCCAGTGCTTAGGGTT 	TGATTCATC: TGATTCATC	9 CAAGATTGGAQAGAGGGGACCGTCAGGGAGAAAATGGCCAQATGATGAGCTGCACATG 	9 TCTTGGGAACGGAAAAGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA	argacataccacgtaggagaacagtggcagaaggaatatctgggtgc 	9 CTGCA.CATGCTTTGGAGGCCAGCGGGGCTTGGCGCTGTGACAACTGCCGCAGACCTGGGGGGTTLTTTTTTTTTT	0 H	9 TCAGAGAACAACAACATATGTTAATTGCCCAATTGAGTGCTTCATGCTTTAGATGTACA 	9 GOCTGACAGAGATTCCCGAGAGTAATCATCTTTCCAATCCAGAGGAACAAGCAIGT	9 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATAGCAGACCCAGCTTAGAGTTCTTC	9 TITCITICITAAGCCCTITGCTCTGGAGG	9 TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCAT	CIGITCTGCTTCGAAGTATTCAATACCGCTCAGTATTTT. 	catatgcagccaacca
658 624	664	636	676	682	688		700	706	712	718	724	730	736	742	748		761

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7381 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7440
728 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
           7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATCTTGTTACTGTGATATTTTAAATATCCA 7788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer.
                                                                                                                                                                                                                                                      Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                   Human breast cancer associated coding sequence SEQ ID NO: 1216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orr MS, Nation M, Diggans JC, Zeng W;
                                                                                                                                                                                                                                                                       cytostatic; gene therapy; gene; ss.
                                                                                                                                                                    ABT11082 standard; cDNA; 7680 BP.
                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001; 2001US-0263757P.
25-APR-2001; 2001US-0286090P.
23-MAY-2001; 2001US-0292517P.
                                                                                                                                                                                                                                                                                                                                                              25-JAN-2002; 2002WO-US002176.
                                                                                                                                                                                                                04-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                              7441 CAGTACT 7447
                                                                                          7789 CAGTACT 7795
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                                                                                                                                                                                                                                                                                                                  WO200259271-A2.
                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         01-AUG-2002.
                                                                                                                                                                                           ABT11082;
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The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more games selected from those shown in ABT09867-ABT1112, where a differential expression of the genes indicates breat cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other; ftp.wipo.int/pub.published_pct_sequences

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Claim 1; SEQ ID NO 1216; 260pp + Sequence Listing; English.

Query Match 95.2%; Score 7423; DB 6; Length 7680; Best Local Similarity 99.8%; Pred. No. 0; Matches 7432; Conservative 0; Mismatches 15; Indels 0; Gaps

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Page 34

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1788 1560 2089 CICAAGIGGICCIGIGGAAGIAITIAICACIGAGACICCGAGICAGCCCAACICCCACCC 2148 1801 carccadiddaargcaccacadccarcrcacarriccaagracarrcraagradaacc 1860 2269 CATCAAAGGCCTGAAGCCTGGTGTGGTATACGAGGGCCAGCTCATCAGCATCCAGCAGTA 2328 2329 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCAGCACCAGCACACCAGCACTGTGAC 2388 1981 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCACCAGCACCAGCACCTCGTGAC 2040 2389 CAGCAACACCGTGACAGAGAGACGACTCCCTTTTTCTCCTTTTTGTGGCCACTTCTGAATC 2448 2449 TGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACACGGT 2508 2101 rereacceanarcacaccacraecrrieresrcrecressrereacricescrices 2509 GTCGGGATTCCCGGGTGGAATATGAGCTGAGTGAGGAGGAAGATGAGCCACAGTACCTGGA 2568 1909 TCACGGTCGGGCGGGTCGAAGTGTGATCCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968 1621 GACGTTTTATCAAATTCGAGATCATGGGAGAAGTATGTGCATGGTGGTGTACAGATACCAGTG 1680 2029 CTACTGCTATGGCCGTGGCATTGGGGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088 1681 cracificitaticacceridecarricesascrateccarcerarcaracacerariceas 1740 1440 1849 GAACGACACATTCCACAAGCGTCATGAAGAGGGGCACATGCTGAACTGTACATGCTTCGG 1908 1549 CAACCACAATTACACTGATTGCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGG 1608 1261 GACCACACAGAACTATGATGCCGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1320 1669 GGAAATCTGCACAACCAATGAAGGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCA 1728 1081 CACAACTTCGAATTATGAGCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTT 1140 1489 GGTTCAGACTCGAGGAGGAAATTCCAATGGTGCCTTGTGCCCACTTCCCCTTCCTATACAA 1548

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antinflammatory steroid, ubiquinone, antiinflammatory, antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC

WO200285308-A2. Homo sapiens.

31-0CT-2002

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6601 CAAGATTGGAGAAGTGGGACCGTCAGGGAAAATGGCCAGATGATGATGAGCTGCACATG 6660
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6949 CAAGATTGGAGAAAGTGGGACCGTCAGGGAGAAAATGGCCAGATGAGGTGACGTGCACATG
                                                                                                                                      TCTTGGGAACGGAAAAGGAGAATTCAAGTGTGACCCTCATGAGGCAACGTGTTACGATGA
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initiation codon, conjugated to object the service of initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 6' or and 3' intron-exon junctions, or regions within 2-10 nucleotides of increase encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubjudinone. A composition of the invention of the antiinflammatory, antiallergic, antisthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or therapeutic respiratory effect of an preventing a respiratory, lung or therapeutic respiratory effect of an artifalammatory steroid in a subject, for reducing levels of adenosine of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of definition.

Cof, or reducing sensitivity to adenosine, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed of the fift and or introducing the printed of the fift and or introducing the printed or presented in the printed or feel fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GACCTACCTAGGTAATGTGTTTGTTTTTTTTTTTTGGAGGAAGCCGAGGTTTTAACTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGANAGTANACCTGANGCTGANGACTTGCTTTGACANGTACACTGGGANCACTTACCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAGCAAGCCCGGTTGTTATGACAATGGAAACACTATCAGATAAATCAACAGTGGGAGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel pharmaceutical composition, which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTACCTAGGCAATGCGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                  Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.2%; Score 7423; DB 7; Length 7680; 99.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 12067; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                     Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                             Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
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Best Local Similarity 99.8†
Matches 7432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-229219/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller S,
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Human; antisense; lung dysfunction; nasal airway dysfunction;

Human nucleic acid sequence.

(first entry)

17-OCT-2003

ABZ96825 standard; DNA; 7680 BP.

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06-AUG-2001; 2001US-0310645P.

(REGC) UNIV CALIFORNIA.

WPI; 2003-278690/27. P-PSDB; ABR81866.

Jarner JA;

Inhibiting angiogenesis in a tissue, useful for treating cancer, arthritis, retinopathy, psoriasis, by providing a tissue and an agent that inhibits specific binding of integrin alpha-4beta-1 to an integrin alpha-4beta-1 ligand.

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6781 CIGCACATGCTTTGGAGGCCAGCGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGG 6840
                                                              6901 TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGACA 6960
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                                          7189 IGAACCCAGTCCCGAAGGCACTACTGGCCAGTCCTACAACCAGTATTCTCAGAGATACCA 7248
                                                                                                                          7249 TCAGAGAACAAACATAATGTTAATTGCCCAATTGAGTGCTTCATGCTTTAGATGTACA 7308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7729 CTGGCCCGCAATACTGTAGGAACAAGCATGATGTTGTTACTGTGATATTTAAATATCCA
                                                                                                                                                                                                                                                                                                                                    7021 CTCTCTGCCAAGATCCATCTAAACTGGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC
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                                                                                                                                                                                                          7309 GGCTGACAGAGAAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGTGT
                                                                                                                                                                                                                                                                                                                                                                            TTTCTTTCTTAAGCCCTTTGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT
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                                                                                                                                                                                                                                                  6961 GGCTGACAGAGATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT
                                                                                                                                                                                                                                                                                            CTCTCTGCCAAGATGCATCTAAACTGGAGTGATGTTAGCAGAGCCCAGCTTAGAGTTCTTC
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The present invention describes a method for inhibiting angiogenesis in a tissue comprising providing a tissue and an agent that inhibits specific tissue comprising providing a tissue and an agent that inhibits specific conditions of integrin alpha4betal to an integrin alpha4betal ligand, and treated treated the tissue with the agent under conditions where the specific binding of the alpha4betal to the ligand is inhibited and a treated tissue is produced. Angiogenesis in the treated tissue is inhibited. Also described: (1) inhibiting endothelial cell adhesion or migration; (2) detecting angiogenesis in a tissue; and is reducting endothelial progenitor cells from a tissue; and (5) reducing symptoms associated with cancer in a subject, or a pathological condition is an ocular or skin tissue. An integrin alpha4betal binding inhibitor symptoms associated with cancer in a subject, or a pathological condition, antifheumatic, antiarthritic, antiinflammatory, osteopathic and dermatological activities, and other pathological condition, such as diabetic returpostry, osteopathic and enthods are useful for treating cancer, and other pathological condition, such as diabetic returpostry.

Concertion by neovascularisation, rheumatoid arthritis, osteoarthritis, of endothelial progentic cells, and in determining the mechanisms that cunderlie angiogenesis, development, wound healing and the function of the female reproductive system: The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468
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Matches 7432; Conservative
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01-AUG-2002; 2002WO-US024573.

402003019136-A2 Homo sapiens.

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                                                                              7021 CTCTGCCAAGAICCATCTAAACTGAGTGATGTTAGCAGACCCAGCTTAGAGTTCTTC 7080
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RESULT 12

ABX10391 standard; DNA; 7680 BP. 4BX10391

28-JAN-2003 (first entry)

DNA encoding protein differentially regulated in prostate cancer #60.

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Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring;

Homo sapiens.

WO200281638-AZ.

17-OCT-2002

08-APR-2002; 2002WO-US010824. 06-APR-2001; 2001US-0281731P (ORIG-) ORIGENE TECHNOLOGIES INC.

06-APR-2001; 2001US-0281732P.

Sun Z, Jay G;

WPI: 2003-058520/05. P-PSDB; ABU07486. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

828 480

421 IGIGIGICTIGGIPALIGGABAAAGGAGAAATIGGACCTGCAAGCCCATAGCTGAGAAAGTTTT

769 TGTGTGTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCCATAGCTGAGAAGTGTTT

Claim 1; Page 136-139; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample comprises the number is indicative of the probability that the sample comprises or prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves context cancer intervention in a subject having a prostate cancer. Which involves the expression levels in a sample comprising prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer calls with a test agent that modulate a biological activity of the polypeptide differentially regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer calls with a test agent where conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, conditions especially relating to prostate cancer. (I) and its seconditions especially relating to prostate cancer. (I) and its subsections in biopsy sample, in total INA, in lymph, in Coloque etc. (I) is useful for assessing cancer eg., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The identification of specific genes, and groups of genes assay for presence of cancer. (I) can also be used for expressing the polypeptide and thus effort asserbing specific genes, and groups of genes postate cancer. The identification of specific genes, and groups of genes postate cancer permits the definition of targets in these partners, and groups of genes and the de prostate cancer

Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

ô 61 AAGCAAGCCCGGTTGTTATGACAATGGAAACACTATCAGATAAATCAACAGTGGGAGCG 120 528 588 240 648 241 AGTGGGTGACTTATGAGGGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 300 708 360 468 768 361 cracaacarregreacaccregaegaegaccacargaeacregregriacarerracarer 420 121 GACCTACCTAGGTAATGTGTTTGGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 180 CTACAAGATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTG 409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG GACCTACCTAGGCAATGCGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTG 529 CGAAAGTAAACCTGAAGCTGAAGACTTGCTTTGACAAGTACACTGGGAACACTTACCG 181 CGAAAGTAAACCTGAAGCTGAAGACTTGCTTTGACAAGTACACTGGGAACACTTAACCG 589 AGTGGGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGG 301 GGCTGGGCGAGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 649 GGCTGGGCGAGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTC 0; Gaps / Match 15:00 Natch 15:2%; Score 7423; DB 7; Length 7680; Local Similarity 99.8%; Pred. No. 0; Local Similarity 99.8%; Pred. No. 0; Mismatches 15; Indels 0; Mismatches 15; Indels 0; Matches 7432; Conservative Query Match

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1009 CAAGAAGGATAATCGAGGAAACCTGCTCCA	TICATCTGCACAGGCAACGCCGAGGAGA 10	q 0	174
1 CAAGAAGGATAATCGAGGAAACC	rrecarcidedadedadedadedadedadedadedadedadedaded	8	214
1069 GTGGAAGTGTGAGAGGCACACACTCTGTGCAG	CAGACCACATCGAGCGGATCTGGCCCCTTCAC 1128	qq	180
CGATGTTCGTGCAGC	CTCACCCCAGCCTCCTCCCTATGGCCA	λδ	220
1 CGAT	PAGCCTCACCCCAGCCTCCTCTATGGCCA 840	අු	186
OTGTGTCACAGACAG	CTGTGGGGATGCAGTGGCTGAAGACACAAGG 1248	λō	226
CTGTGT	CTGTGGGGATGCAGTGGTTGAAGACACAAGG	අ <u>ධ</u>	192
3CAAATGCTTTGCACGTGC	CTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGT 1308	73 - 41	1981
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OB AACCCA	GACTTACGGTGGCAACTCAAATGGAGAGCCATGTGTCTTACCATTCACCTACAA 1368	ପ୍ର	204
AACCCA	142	ò	244
21 TGGCAGGACGTTCTACTCCTGCACCA	CGGAAGGCCACACGACGACATCTTTGGTGCAC 1080	q ₀	2101
CACAACTTCGAATTATGAGCAGGACCA	m	₹ 6 	216
081 CACAACTTCG	rgcacagaccacactgrrrr 114	à	256
1489 GGTTCAGACTCGAGGAAATTCCAATGGTGCTTGTGC 1141 GGTTCACACTCBAGGAGAAATTCCAATGGTGCCTTGTGC	GGTGCCTTGTGCCACTTCCCTTCCTATACAA 1548	q a	222
9 CAACCACAAT	SACAACATGAAC	<i>ኤ</i>	2629
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609 GA	AAGTTTGGGTTCTGCCCCATGGCTGCCCACGA 1668	ପୁ	2341
261 GACCACAGAACTATGATGCCGAC	STITGGGTTCTGCCCCATGGCTGCCCACGA 13Z	ò	2749
69 GGAAATCTGCACAACCAATGAAGGGGT	CATGIACCGCAIIGGAGAICAGIGGGAIAAGCA 1/20	qa	2401
21 GGAATICIGCACCAAIGAAGGGGI	ACCGCA11GGAGAICAGIGGGAIAAGCA 1500	ò	2809
729 GCATGACATGGGTCACATGATGAGGTG	CACGTGTGTTGGGAATGGTCGTGGGGAATGGG 1788	qa	246:
81 GCATGACATGGGTCACATGATGAGGTGC		۸۵	286
ATGCATTGCCTACTCGCAGCTTCGAGAT	AGIGCATIGITGAIGACAICACITACAATGI 10	qu	252
1441 AIGCAITGCCIACICGCAACIICGAGAIC	9 6	00	292
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9 AGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACCCCAGGCTCAGATACAGT 2988 Griceechtriceecheeantardaecheacheacheacheacheacheacherachea 2220 Aacaacaacaccidarioccccrccrcacccaacrigiogaccaacircaacaccccaar 2400 refricacideadcadaccccadeciccarcadaedadaaaaaaradicariricacc 2460 9 GCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGAAGGTCACCATCATGTG 3048 ceschicaasaasastescricecriridacrirdaccaccaccaccaccaccacacacacacarers TCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGACCTGCTTCCTGGCCGAAAATACAT 2628 TGTAAATGTCTATCAGATATCTGAGGAAGCAGAGTTTGATCCTGTCTACTTCACA 2688 TGTTGTTCGCTGGAGCAGACCCCCAGGCTCCCATCACAGGGTACAGAATAGTCTATTCGCC 2808 ATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAACTGCAAACTCCGTCACCCT 2868 gacerrirarcaaarregacarrearegacaagaagrareregearegrereagaraceagre 1680 CTCAAGTGGTCCTGTCGAAGTATTTATCACTGAGACTCCGAGTCAGCCCAACTCCCACCC 2148 CATCCAGTGGAATGCACCACCATCTCACATTTCCAAGTACATTCTCAGGTGGAGACC 2208 carccagregaarecaccaccarcreacarrirecaagracarrercageacagregae TAAAAATTCTGTAGGCCGTTGGAAGGAAGCTACCATACCAGGCCACTTAAACTCCTACAC 2268 CATCAAAGGCCTGAAGCCTGGTGTGTGTATACGAGGCCAGCTCATCAGCATCCAGCAGTA 2328 CGGCCACCAAGAAGTGACTCGCTTTGACTTCACCACCACCACCAGCACCAGCACCTGTGAC 2388 CAGCAACACCGTGACAGGAGAGGACGACTCCCTTTTCTCCTCTTGTGGCCACTTCTGAATC 2448 TGTGACCGAAATCACAGCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGT 2508 rereacceaaarcacaeceaeraecrrreresercrecereeercreserresecreeer 2160 GICGGGAITCCGGGIGGAAIAIGAGCIGAGIGAGGAGAGAIGAGCCACAGIACCIGGA 2568 rerakarchercharchererengardedeaceacherrhearccherchachea 2340 CTACTGCTATGGCCGTGGCATTGGCGAGTGGCATTGCCAACCTTTACAGACCTATCCAAG 2088 CICAAGIGGICCIGICGAAGIAITITAICACIGAGACICCGAGICAGCCCAACICCCACCC 1800 1909 TCAGGGTCGGGGAGGTGGAAGTGTGATCCCGTCGACCAATGCCAGGATTCAGAGACTGG 1968 GACGITITATCAAATIGGAGATICATGGGAGAAGTATGTGCATGGTGTCAGATACCAGTG 2028 AACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGACCAAGTTGATGACACCTCAAT arcagradaaagaragcacagaacrcaaccrrccrgaaacrgcaaacrccgrcacccr

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ACC46009 standard; DNA; 7680 BP. (first entry) Human fibronectin gene FN. 02-JUN-2003 ACC46009 RESULT

Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strangth; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporcsis; esteomalacia; rickets; Paget's disease; neoplasm of the bone; gene; ds.

Homo sapiens.

WO200292764-A2

13-MAY-2002; 2002WO-US014876. 21-NOV-2002.

11-MAY-2001; 2001US-0290071F. 17-MAY-2001; 2001US-029111P. 01-FEB-2002; 2002US-0353058P. 04-MAR-2002; 2002US-0361293F.

(GENO-) GENOME THERAPEUTICS CORP (AMHP) WYETH. sabij P, Bex FJ, Yaworsky PJ, Bodine PV;

WPI; 2003-129278/12.

New transgenic animals (e.g. mice), useful as models for studying bone density modulation, developing drugs for treating or preventing bone diseases (e.g. osteoporosis), or diagnosing diseases characterized by reduced bone density.

Disclosure; Page 498-501; 603pp; English.

1009 CAAGAAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGA 1068

601 TAGAAATAGATGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAG 660

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The invention relates to novel transgenic animals expressing the high bone mass (HBM) gene, expressing the corresponding wild type HBM gene, comprising an alteration of the gene encoding LRP6, or expressing an IRP5 that is modulated by an altered gene control sequence introduced an LRP5 that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are convention may not an expectatic activity. The polynucleotides of invention may have a use in gene therapy. The transgenic animals and cucleic acids are for the study of bone classity modulation. Where the bone mass is modulated relative to non-transgenic animals and composition may have a use in gene therapy. The transgenic animals and concerns in more than one parameter selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals, mucleic acids and methods are useful for identifying compositions, which may be employed for treating or preventing bone diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also useful in methods for disposing diseases in bone development, or characterised by reduced bone density or mass. The present sequence is used in the exemplification of the invention
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Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;

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ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I) given in ABR92047 to ABR92164. A higher level of expression of (I) than normal indicates the presence of cervical cancer. Also described: (I) a vector (II) containing (I); (2) a host call (III) containing (I); and (3) assessing (MI) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a patient's cample, and the normal level of expression of the marker in a control non-cervical cancer sample, where a significant increase in the level of expression of the marker in the patient's sample relative to that in the cervical cancer. (I) has cytostatic activity, and can be used in gene therapy and in vaccines. (I) is useful in detecting, characterising, therapy and in vaccines. (I) is useful in detecting, characterising, various prognostic and diagnostic assays, pharmacogenomics and in varials
                                                   7669 GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
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diagnostic assays, in pharmacogenomics and in monitoring clinical trials
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This invention describes a novel reagent for diagnosis, molecular definition and therapy of chronic inflammatory joint diseases, and other inflammatory disorders, infective or tumour diseases in humans. The products of the invention have antilnflammatory, cytostatic, antirheumatic and immunosuppressive activity and can be used for gene therapy. The reagent of the invention and any proteins and antibodies derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation, chronic joint diseases, on the basis of molecular characterisation, and electronic joint diseases, not the basis of molecular characterisation, and the termining the etiological pathogenicity principle of as yet uncharacterised inflammatory diseases, also monitoring progression and/or treatment of disease, and optimisation of therapy and (iii) for developing treatments for inflammatory diseases, particularly of joints, infections and tumours. Acade4801-Acade4965 represent human polynucleotides used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCG
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                                                                                                                            Human, chronic inflammatory joint disease, infection, tumour, antiinflammatory, cytostatic, antiarthritic, antirheumatic, immunosuppressive, gene therapy, etiological pathogenicity, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7680 BP; 2081 A; 1981 C; 1862 G; 1756 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 95.2%; Score 7423; DB 7; Length 7
Similarity 99.8%; Pred. No. 0;
32; Conservative 0; Mismatches 15; Indels
                                                                                   Human fibronectin DNA corresponding to X02761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haeupl T, Ungethuem U, Blaess S;
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                                           27-JUN-2003 (first entry)
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	TACAGGGT 	4981 AGAGCTGCAAGGCCTCAGACCGGGTTCTGAGTACACAGTCAGT	TCAGCTCACTGGATATCGAGTGGCGCGCCAAGGAGAAGACCGGACCAATGAAAGA 556	\$629 ATATGAAGTGACTGTCTTAAGGACACTTTGACAAGCAGACCAGCTCAGGGAGT 5688	GACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGA GACCACCATCACCATTAGCTGGAGAACCAAGACGAACGATCACTGGCTTCCAAGTTGA TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAAG TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAAGCATCAAGCCAGATGTCAGAAG TGCCGTTCCAGCCAATGGCCAGACTCCAATCCAGAGAACCATCAAGCCAGATGTCAGAAG TGCCGTTCACAGCAATGGCCAGACTACAAGATCTACCTGTACCTTGAA	521 CTACACCATCACAGGTTTACAACCAGGACTGACTACAAGATCTACCTGTACATGAA 929 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCCATTGATGCACCTTGAA 581 TGACAATGCTCGGAGCTCCCCTGTGGTCATCGACGCCTCCCATTGATGCACCATC	641 CAACCTGGGTTTCCTGGCCACCCCAATTCCTTGCTGGTATCATGGCAGCCCCCCGG 649 TGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTATCCTTCCT
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109 GGTCCCTCGGCCCGCCCTGGTGTCACAGAGGCTACTATTACTGGCCTGGAACCGGGAAC 	atacaatttatgtcattgccctgaagaataatcagaagaggggggcccctgattgg 	arararcagacgagcticcccaactggtaacccticcacaccccaatcticatgg 	ACAGITCAAAAGACCCTITCGICACCCACCCTGG	349 GTATGACACTGGAAATGGTATTCAGCTTCCTGGCACTTCTGGTCAGCAACCCAGTGTTGG 	aratgrictttgrggarcriggttttrggcgarccacaccgccca 	6469 CCCCATAAGGCATAGGCCAAGACCATACCCGCCGAATGTAGGACAAGAAGCTCTCTCT	6529 GAGAACCATCTCATGGGCCCCATTCCAGGACACTTCTGAGTACATCATTCAT	6589 TGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTTCTACCAGTGCCAC 	6649 TCTGACAGGCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACCA 	6709 GCAGAGGCATAAAGGTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTT 	6769 GAACCAACCTACGGATGACTCGTGCTTTGACCCCTACACAGTGTCCCATTATGCCGTTGG	6829 AGAIGAGIGAGAACGAAIGICIGAATCAGGCITIAAACIGIIGIGCCAGIGCITAGGCIT 	6889 TGGAAGTGGTCATTTCAGATGTGATTCATCTAGATGGTGCCATGACAATGGTGTGAACTA 	6949 CAAGAITGGAGAAAGTGGGACCGICAGGGAGAAAATGGCCAGATGAIGAGCTGCACAIG 	aaggagaatto aaggagaatto	7069 TGGGAAGACATACCACGTAGGAGAAACAGTGGCAGAAGGAATATCTCGGTGCCATTTGCTC	GAGGCCAGGGGGCTGGCGCTGTGACAACTG

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ò	7249	TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 7308
qq	6901	TCAGAGAACAAACACTAATGTTAATTGCCCAATTGAGTGCTTCATGCCTTTAGATGTACA 6960
λ	7309	GGCTGACAGAGAATTCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7368
엄	6961	GCCTGACAGAGAAGATTCCCCGAGAGTAAATCATCTTTCCAATCCAGAGGAACAAGCATGT 7020
ò	7369	CICTCIGCCAAGAICCAICTAAACIGGAGIGTIAGGAGAGACCCAGCTIAGAGITCIIC 7428
qq	7021	CTCTCTGCCAAGATCCATCTAAACTGGAGTGATTAGCAGACCCAGCTTAGAGTTCTTC 7080
δ	7429	TITCITICITAAGCCCITIGCICIGGAGGAAGITCICCAGCTICAGCICAACICAA
qq	7081	TITCTITCTIAAGCCCTITGCTCTGGAGGAAGTTCTCCAGCTTCAGCTCAACTCACAGCT 7140
ò	7489	TCTCCAAGCATCACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATT 7548
Д	7141	TCTCCAAGCATCACCCTGGGAGTTTTCTCATAATGAGGCTGCACATT 7200
δ	7549	GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7608
ag Q	7201	GCCTGTTCTGCTTCGAAGTATTCAATACCGCTCAGTATTTTAAATGAAGTGATTCTAAGA 7260
ò	7609	TITGGITIGGGATCAATAGGAAAGCATATGCAGCCAAGATGCAAAATGTITIGAAAT 7668
dū	7261	TTTGGTTTTGGGATCATAGGAAAGCATATGCAGCCAACCAA
ò	7669	GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7728
qq	7321	GATATGACCAAAATTTTAAGTAGGAAAGTCACCCAAACACTTCTGCTTTCACTTAAGTGT 7380
ò	7729	
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